

STIC-Biotech/ChemLib

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From: Collins, Cynthia  
Sent: Monday, March 24, 2003 12:56 PM  
T : STIC-Biotech/ChemLib  
Subject: sequence search request SN 09/856725

Please do an OLIGO search, **both** prior art and interference, for SN 09/856725:

1) SEQ ID NO:2

Thank You,

Cynthia Collins  
Art Unit 1638  
CM1, 9A12 (office) or 9E12 (mailbox)  
(703) 605-1210

Point of Contact:  
Beverly Shears  
Technical Info. Specialist  
CM1 1E05 Tel: 308-4994

PCT 9/25/00

6/14/04

Gentile  
#3

Dec 498  
their US patent

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
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Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
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Other (specify): \_\_\_\_\_

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# SEARCH REQUEST FORM

Requestor's

Name: \_\_\_\_\_

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Number: \_\_\_\_\_

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Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 04-04-03

Searcher: Beverly e 4994

Terminal time: 20

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: 23

Number of Searches: \_\_\_\_\_

Number of Databases: 1

### Search Site

\_\_\_\_\_ STIC

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### Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_\_ IG Suite

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 11:33:28 ; Search time 2218 Seconds  
(without alignments)  
6960.094 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 1000 summaries

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## SUMMARIES

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C 365	18	2.9	224	65	US-60-217-080-876	Sequence 876, App	437	18	2.9	301	30	US-09-785-216A-60655	Sequence 60655, A
C 366	18	2.9	231	30	US-09-785-276A-60129	Sequence 60129, A	438	18	2.9	306	36	US-09-969-373-1187	Sequence 1187, Ap
C 367	18	2.9	243	16	US-09-244-000A-90744	Sequence 90744, A	439	18	2.9	309	62	US-60-185-215-1295	Sequence 1295, Ap
C 368	18	2.9	243	17	US-09-304-517A-139322	Sequence 139322, A	440	18	2.9	311	19	US-09-521-640-13519	Sequence 13519, A
C 369	18	2.9	243	17	US-09-371-146A-139322	Sequence 139322, A	441	18	2.9	314	60	US-60-164-378-12	Sequence 12, Appl
C 370	18	2.9	243	25	US-09-654-617-43445	Sequence 43445, A	442	18	2.9	316	24	US-09-637-088A-39349	Sequence 39349, A
C 371	18	2.9	243	36	US-09-978-703-90744	Sequence 43445, A	443	18	2.9	316	24	US-09-637-086D-39349	Sequence 39349, A
C 372	18	2.9	243	37	US-09-985-678-139322	Sequence 90744, A	444	18	2.9	316	25	US-09-654-617-249003	Sequence 249003, A
C 373	18	2.9	245	25	US-09-985-678-139322	Sequence 139322, A	445	18	2.9	316	25	US-09-654-617-249003	Sequence 249003, A
C 374	18	2.9	245	27	US-09-654-617-379188	Sequence 379188, A	446	18	2.9	317	23	US-09-605-700-17768	Sequence 17768, A
C 375	18	2.9	246	16	US-09-684-016-379188	Sequence 379188, A	447	18	2.9	318	19	US-09-521-640-34604	Sequence 34604, A
C 376	18	2.9	246	34	US-09-923-876-2923	Sequence 2923, Ap	448	18	2.9	328	16	US-09-231-945-2245	Sequence 2245, Ap
C 377	18	2.9	249	18	US-09-420-691-2137	Sequence 2923, Ap	449	18	2.9	328	21	US-09-540-213-52937	Sequence 52937, A
C 378	18	2.9	249	21	US-09-540-213-47250	Sequence 47250, A	450	18	2.9	336	19	US-09-521-640-125308	Sequence 125308, A
C 379	18	2.9	249	21	US-09-540-499-24266	Sequence 24266, A	451	18	2.9	337	19	US-09-521-640-125271	Sequence 125271, A
C 380	18	2.9	249	21	US-09-540-499B-24266	Sequence 24266, A	452	18	2.9	341	17	US-09-304-517A-270397	Sequence 270397, A
C 381	18	2.9	249	54	US-60-108-396-230	Sequence 24266, A	453	18	2.9	341	17	US-09-371-146A-269236	Sequence 269236, A
C 382	18	2.9	251	13	US-08-962-919-3684	Sequence 230, App	454	18	2.9	341	22	US-09-565-240-17072	Sequence 17072, A
C 383	18	2.9	251	13	US-08-962-919-3684	Sequence 3684, Ap	455	18	2.9	343	37	US-09-985-678-275097	Sequence 270397, A
C 384	18	2.9	251	20	US-09-535-897-43737	Sequence 43737, A	456	18	2.9	343	19	US-09-521-640-170497	Sequence 170497, A
C 385	18	2.9	252	47	US-60-036-400-899	Sequence 899, App	457	18	2.9	345	16	US-09-289-768-9754	Sequence 9754, Ap
C 386	18	2.9	253	23	US-09-605-700-18685	Sequence 18685, A	458	18	2.9	345	25	US-09-654-617-382659	Sequence 432659, A
	18	2.9	253	18	US-09-436-762A-11326	Sequence 11326, A	459	18	2.9	345	26	US-09-669-817A-38430	Sequence 38430, A

C 460	18	2.9	345	27	US-09-684-016-432659	Sequence 432659, A	C 533	18	2.9	406	24	US-09-637-086A-23839	Sequence 23839, A
C 461	18	2.9	345	35	US-09-939-397-9754	Sequence 9754, Ap	C 534	18	2.9	406	24	US-09-637-086D-23839	Sequence 23839, A
C 462	18	2.9	346	63	US-60-197-872-63562	Sequence 63562, A	C 535	18	2.9	406	25	US-09-654-617-245040	Sequence 245040, A
C 463	18	2.9	348	5	US-08-104-507A-5244	Sequence 5244, Ap	C 536	18	2.9	406	27	US-09-684-016-245040	Sequence 245040, A
C 464	18	2.9	348	5	US-08-104-507C-5244	Sequence 5244, Ap	C 537	18	2.9	410	25	US-09-654-617-134883	Sequence 134883, A
C 465	18	2.9	351	80	US-60-360-207-26048	Sequence 26048, A	C 538	18	2.9	410	27	US-09-684-016-134883	Sequence 134883, A
C 466	18	2.9	355	16	US-09-270-849B-175454	Sequence 175454, A	C 539	18	2.9	411	16	US-09-293-972-19392	Sequence 19392, A
C 467	18	2.9	361	14	US-09-076-897-6696	Sequence 6696, Ap	C 540	18	2.9	411	16	US-09-293-972-19392	Sequence 19392, A
C 468	18	2.9	361	14	US-09-076-897A-6696	Sequence 6696, Ap	C 541	18	2.9	413	17	US-09-359-067-43233	Sequence 43233, A
C 469	18	2.9	361	14	US-09-076-897B-6696	Sequence 6696, Ap	C 542	18	2.9	413	63	US-60-197-872-51401	Sequence 51401, A
C 470	18	2.9	361	14	US-09-076-897C-6696	Sequence 6696, Ap	C 543	18	2.9	417	18	US-09-480-992-12649	Sequence 12649, A
C 471	18	2.9	361	24	US-09-625-102-1309	Sequence 1309, Ap	C 544	18	2.9	417	36	US-09-960-352-12649	Sequence 12649, A
C 472	18	2.9	362	28	US-09-704-424-6728	Sequence 6728, Ap	C 545	18	2.9	423	17	US-09-317-311C-941	Sequence 941, App
C 473	18	2.9	364	19	US-09-521-640-6827	Sequence 6827, Ap	C 546	18	2.9	423	39	US-10-077-478-941	Sequence 941, App
C 474	18	2.9	368	19	US-09-521-640-85431	Sequence 85431, A	C 547	18	2.9	424	19	US-09-521-640-145341	Sequence 145341, A
C 475	18	2.9	368	25	US-09-654-617-166465	Sequence 166465, A	C 548	18	2.9	424	24	US-09-637-086A-22499	Sequence 22499, A
C 476	18	2.9	368	27	US-09-684-016-166465	Sequence 166465, A	C 549	18	2.9	424	24	US-09-637-086D-22499	Sequence 22499, A
C 477	18	2.9	370	17	US-09-362-510-16131	Sequence 16131, A	C 550	18	2.9	424	25	US-09-654-617-244679	Sequence 244679, A
C 478	18	2.9	370	17	US-09-362-510A-16131	Sequence 16131, A	C 551	18	2.9	424	25	US-09-654-617-244679	Sequence 244679, A
C 479	18	2.9	370	34	US-09-904-013-16131	Sequence 16131, A	C 552	18	2.9	424	27	US-09-684-016-244679	Sequence 244679, A
C 480	18	2.9	370	63	US-60-197-872-22253	Sequence 22253, A	C 553	18	2.9	425	24	US-09-621-976-8173	Sequence 8173, Ap
C 481	18	2.9	372	23	US-09-606-680-138	Sequence 138, App	C 554	18	2.9	425	32	US-09-849-556A-3236	Sequence 3236, Ap
C 482	18	2.9	375	17	US-09-304-517A-263588	Sequence 263588, A	C 555	18	2.9	425	58	US-60-147-499-8173	Sequence 8173, Ap
C 483	18	2.9	375	17	US-09-371-146A-262548	Sequence 262548, A	C 556	18	2.9	428	64	US-60-203-214-3236	Sequence 3236, Ap
C 484	18	2.9	375	18	US-09-440-687-16718	Sequence 16718, A	C 557	18	2.9	430	69	US-60-253-652-6049	Sequence 6049, Ap
C 485	18	2.9	375	37	US-09-985-678-263588	Sequence 263588, A	C 558	18	2.9	430	17	US-09-304-517A-270598	Sequence 270598
C 486	18	2.9	375	58	US-60-144-084-21101	Sequence 21101, A	C 559	18	2.9	430	22	US-09-371-146A-269436	Sequence 269436
C 487	18	2.9	376	17	US-09-362-510-57107	Sequence 57107, A	C 560	18	2.9	430	37	US-09-985-678-270598	Sequence 270598
C 488	18	2.9	376	17	US-09-362-510A-57107	Sequence 57107, A	C 561	18	2.9	435	22	US-09-572-409-33556	Sequence 33556, A
C 489	18	2.9	376	24	US-09-637-086A-50752	Sequence 50752, A	C 562	18	2.9	436	16	US-09-271-450-16271	Sequence 16271, A
C 490	18	2.9	376	24	US-09-637-086D-50752	Sequence 50752, A	C 563	18	2.9	436	34	US-09-925-552-16271	Sequence 16271, A
C 491	18	2.9	376	25	US-09-654-617-253632	Sequence 253632, A	C 564	18	2.9	436	38	US-10-033-354-16271	Sequence 16271, A
C 492	18	2.9	376	27	US-09-684-016-253632	Sequence 253632, A	C 565	18	2.9	437	12	US-08-803-609-1000	Sequence 1000, Ap
C 493	18	2.9	376	34	US-09-904-013-57107	Sequence 57107, A	C 566	18	2.9	437	19	US-09-521-640-66510	Sequence 66510, A
C 494	18	2.9	378	18	US-09-436-762A-9277	Sequence 9277, Ap	C 567	18	2.9	437	34	US-09-912-292-5573	Sequence 5573, Ap
C 495	18	2.9	379	26	US-09-666-355A-4460	Sequence 4460, Ap	C 568	18	2.9	438	18	US-09-421-106-19926	Sequence 19926, A
C 496	18	2.9	386	19	PCT-US01-01334-1705	Sequence 1705, Ap	C 569	18	2.9	438	19	US-09-521-640-288402	Sequence 288402, A
C 497	18	2.9	386	19	US-09-521-640-246370	Sequence 246370, A	C 570	18	2.9	438	22	US-09-552-087-16868	Sequence 16868, A
C 498	18	2.9	386	30	US-09-764-874-1705	Sequence 1705, Ap	C 571	18	2.9	438	22	US-09-552-087B-16868	Sequence 16868, A
C 499	18	2.9	386	39	US-10-092-400-1705	Sequence 1705, Ap	C 572	18	2.9	438	23	US-09-605-770-17978	Sequence 17978, A
C 500	18	2.9	387	33	US-09-865-439A-7591	Sequence 7591, Ap	C 573	18	2.9	439	17	US-09-399-770-18932	Sequence 18932, A
C 501	18	2.9	389	19	US-09-521-640-141676	Sequence 141676, A	C 574	18	2.9	439	23	US-09-605-700-17995	Sequence 17995, A
C 502	18	2.9	391	25	US-09-654-617-166518	Sequence 166518, A	C 575	18	2.9	440	34	US-09-921-378-18932	Sequence 18932, A
C 503	18	2.9	391	27	US-09-684-016-166518	Sequence 166518, A	C 576	18	2.9	440	19	US-09-521-640-87799	Sequence 87799, A
C 504	18	2.9	392	17	US-09-394-745-11055	Sequence 11055, A	C 577	18	2.9	442	20	US-09-534-854-4909	Sequence 4909, Ap
C 505	18	2.9	392	19	US-09-528-409-104897	Sequence 104897, A	C 578	18	2.9	445	16	US-09-293-972-11081	Sequence 11081, A
C 506	18	2.9	392	22	US-09-565-306-29540	Sequence 29540, A	C 579	18	2.9	445	18	US-09-471-277-5107	Sequence 5107, Ap
C 507	18	2.9	392	35	US-09-933-524A-104897	Sequence 104897, A	C 580	18	2.9	445	18	US-09-904-939-11081	Sequence 11081, A
C 508	18	2.9	392	35	US-09-933-524A-104897	Sequence 104897, A	C 581	18	2.9	448	19	US-09-528-409-31463	Sequence 31463, A
C 509	18	2.9	393	17	US-09-359-067-26621	Sequence 26621, A	C 582	18	2.9	448	35	US-09-933-554A-31463	Sequence 31463, A
C 510	18	2.9	396	17	US-09-362-510-20588	Sequence 20588, A	C 583	18	2.9	448	35	US-09-933-554A-31463	Sequence 31463, A
C 511	18	2.9	396	17	US-09-362-510A-20588	Sequence 20588, A	C 584	18	2.9	453	17	US-09-362-510A-1957	Sequence 1957, Ap
C 512	18	2.9	396	34	US-09-904-013-20588	Sequence 20588, A	C 585	18	2.9	453	17	US-09-362-510A-1957	Sequence 1957, Ap
C 513	18	2.9	397	16	US-09-293-972-31035	Sequence 31035, A	C 586	18	2.9	453	34	US-09-904-013-1957	Sequence 1957, Ap
C 514	18	2.9	397	34	US-09-904-939-31035	Sequence 31035, A	C 587	18	2.9	453	80	US-60-360-207-25734	Sequence 25734, A
C 515	18	2.9	397	80	US-60-360-207-32748	Sequence 32748, A	C 588	18	2.9	460	39	US-10-098-754-10224	Sequence 10224, A
C 516	18	2.9	398	19	US-09-521-640-110511	Sequence 110511, A	C 589	18	2.9	468	18	US-09-442-106-773	Sequence 773, App
C 517	18	2.9	400	1	PCT-US01-01334-10459	Sequence 10459, A	C 590	18	2.9	468	19	US-09-521-640-152680	Sequence 152680, A
C 518	18	2.9	400	1	PCT-US01-01334-10460	Sequence 10460, A	C 591	18	2.9	473	24	US-09-628-857-618	Sequence 618, App
C 519	18	2.9	400	1	PCT-US01-01334-10461	Sequence 10461, A	C 592	18	2.9	473	34	US-09-912-292-39157	Sequence 39157, A
C 520	18	2.9	400	22	US-09-565-306-66833	Sequence 66833, A	C 593	18	2.9	478	32	US-09-834-366-28012	Sequence 28012, A
C 521	18	2.9	400	22	US-09-565-306-66833	Sequence 66833, A	C 594	18	2.9	478	63	US-60-197-873-28012	Sequence 28012, A
C 522	18	2.9	400	30	US-09-764-874-10459	Sequence 10459, A	C 595	18	2.9	479	19	US-09-521-640-220982	Sequence 220982, A
C 523	18	2.9	400	30	US-09-764-874-10460	Sequence 10460, A	C 596	18	2.9	479	24	US-09-621-976-8278	Sequence 8278, Ap
C 524	18	2.9	400	30	US-09-764-874-10461	Sequence 10461, A	C 597	18	2.9	479	58	US-60-140-769-27001	Sequence 27001, A
C 525	18	2.9	400	39	US-10-092-400-10459	Sequence 10459, A	C 598	18	2.9	479	58	US-60-147-499-8278	Sequence 8278, Ap
C 526	18	2.9	400	39	US-10-092-400-10460	Sequence 10460, A	C 599	18	2.9	480	22	US-09-565-309A-21673	Sequence 21673, A
C 527	18	2.9	400	39	US-10-092-400-10461	Sequence 10461, A	C 600	18	2.9	482	19	US-09-521-640-270166	Sequence 270166, A
C 528	18	2.9	401	14	US-09-076-897-6678	Sequence 6678, Ap	C 601	18	2.9	484	19	US-09-521-640-223565	Sequence 223565, A
C 529	18	2.9	401	14	US-09-076-897A-6678	Sequence 6678, Ap	C 602	18	2.9	484	19	US-09-528-409-29986	Sequence 29986, A
C 530	18	2.9	401	14	US-09-076-897B-6678	Sequence 6678, Ap	C 603	18	2.9	484	35	US-09-933-554-29986	Sequence 29986, A
C 531	18	2.9	401	14	US-09-076-897C-6678	Sequence 6678, Ap	C 604	18	2.9	484	35	US-09-933-554A-29986	Sequence 29986, A
C 532	18	2.9	402	22	US-09-572-409-47771	Sequence 47771, A	C 605	18	2.9	489	30	US-09-770-961-709	Sequence 709, App

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C 607	18	2.9	490	35	US-09-932-076-1590	Sequence 1390, Ap
C 608	18	2.9	492	80	US-60-360-207-26874	Sequence 26874, A
C 609	18	2.9	493	33	US-09-874-708A-16618	Sequence 16618, A
C 610	18	2.9	493	65	US-60-211-750-16475	Sequence 16475, A
C 611	18	2.9	494	32	US-09-850-147-5775	Sequence 5775, Ap
C 612	18	2.9	494	64	US-60-202-213-5592	Sequence 5592, Ap
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C 614	18	2.9	497	25	US-09-652-355-770	Sequence 770, App
C 615	18	2.9	498	24	US-09-634-306B-266519	Sequence 266519, A
C 616	18	2.9	498	24	US-09-637-086A-26283	Sequence 26283, A
C 617	18	2.9	498	24	US-09-637-086D-26283	Sequence 26283, A
C 618	18	2.9	498	38	US-10-027-632-266519	Sequence 266519, A
C 619	18	2.9	502	19	US-09-538-409-95204	Sequence 95204, A
C 620	18	2.9	502	24	US-09-634-306B-60205	Sequence 60205, A
C 621	18	2.9	502	24	US-09-634-306B-298575	Sequence 298575, A
C 622	18	2.9	502	35	US-09-933-524-95204	Sequence 95204, A
C 623	18	2.9	502	35	US-09-933-524A-95204	Sequence 95204, A
C 624	18	2.9	502	38	US-10-027-632-60205	Sequence 60205, A
C 625	18	2.9	502	38	US-10-027-632-298575	Sequence 298575, A
C 626	18	2.9	503	43	US-10-260-238-5061	Sequence 5061, Ap
C 627	18	2.9	504	24	US-09-634-306B-43037	Sequence 43037, A
C 628	18	2.9	504	38	US-10-027-632-43037	Sequence 43037, A
C 629	18	2.9	507	24	US-09-634-306B-98352	Sequence 98352, A
C 630	18	2.9	507	33	US-09-874-708A-80541	Sequence 80541, A
C 631	18	2.9	507	38	US-10-027-632-98352	Sequence 98352, A
C 632	18	2.9	507	65	US-60-211-750-79408	Sequence 79408, A
C 633	18	2.9	508	24	US-09-634-306B-266520	Sequence 266520, A
C 634	18	2.9	508	24	US-09-634-306B-266521	Sequence 266521, A
C 635	18	2.9	508	38	US-10-027-632-266520	Sequence 266520, A
C 636	18	2.9	508	38	US-10-027-632-266521	Sequence 266521, A
C 637	18	2.9	509	38	US-60-278-332-3150	Sequence 3150, Ap
C 638	18	2.9	513	22	US-09-565-309A-18534	Sequence 18534, A
C 639	18	2.9	514	16	US-09-240-371-6397	Sequence 6397, Ap
C 640	18	2.9	514	16	US-09-293-972-5816	Sequence 5816, Ap
C 641	18	2.9	514	24	US-09-634-306B-324397	Sequence 324397, A
C 642	18	2.9	514	24	US-09-634-306B-324398	Sequence 324398, A
C 643	18	2.9	514	34	US-09-904-939-5816	Sequence 5816, Ap
C 644	18	2.9	514	34	US-09-919-724-6397	Sequence 6397, Ap
C 645	18	2.9	514	38	US-10-027-632-324397	Sequence 324397, A
C 646	18	2.9	514	38	US-10-027-632-324398	Sequence 324398, A
C 647	18	2.9	517	28	US-09-705-926-3834	Sequence 3834, Ap
C 648	18	2.9	520	19	US-09-505-532-36918	Sequence 36918, A
C 649	18	2.9	520	31	US-09-819-091A-36918	Sequence 36918, A
C 650	18	2.9	520	31	US-09-819-091A-36918	Sequence 36918, A
C 651	18	2.9	530	22	US-09-649-165A-7672	Sequence 7672, Ap
C 652	18	2.9	530	22	US-09-565-240-50403	Sequence 50403, A
C 653	18	2.9	535	33	US-09-865-439A-98105	Sequence 98105, A
C 654	18	2.9	535	64	US-60-207-458-142026	Sequence 142026, A
C 655	18	2.9	536	1	PCT-US00-09437-350	Sequence 350, App
C 656	18	2.9	536	21	US-09-543-668-350	Sequence 350, App
C 657	18	2.9	536	37	US-09-991-936-350	Sequence 350, App
C 658	18	2.9	539	18	US-09-471-277-5408	Sequence 5408, Ap
C 659	18	2.9	541	24	US-09-634-306B-4950	Sequence 4950, Ap
C 660	18	2.9	541	24	US-09-634-306B-4951	Sequence 4951, Ap
C 661	18	2.9	541	38	US-10-027-632-4950	Sequence 4950, Ap
C 662	18	2.9	541	38	US-10-027-632-4951	Sequence 4951, Ap
C 663	18	2.9	543	32	US-09-849-529A-18207	Sequence 18207, A
C 664	18	2.9	543	63	US-60-196-868-18191	Sequence 18191, A
C 665	18	2.9	545	30	US-09-770-152-606	Sequence 606, App
C 666	18	2.9	546	80	US-60-360-207-28944	Sequence 28944, A
C 667	18	2.9	548	24	US-09-629-469A-1869	Sequence 5869, Ap
C 668	18	2.9	553	24	US-09-629-469A-1869	Sequence 5869, Ap
C 669	18	2.9	553	38	US-10-027-632-180614	Sequence 180614, A
C 670	18	2.9	559	24	US-09-634-306B-246682	Sequence 246682, A
C 671	18	2.9	559	38	US-10-027-632-246682	Sequence 246682, A
C 672	18	2.9	559	38	US-10-027-632-246683	Sequence 246683, A
C 673	18	2.9	561	19	US-09-505-532-9486	Sequence 9486, Ap
C 674	18	2.9	561	31	US-09-819-091A-9486	Sequence 9486, Ap
C 675	18	2.9	562	33	US-09-865-439A-77374	Sequence 77374, A
C 676	18	2.9	562	64	US-60-207-458-11516	Sequence 11516, A
C 677	18	2.9	566	25	US-09-654-617-15730	Sequence 15730, A
C 678	18	2.9	566	27	US-09-684-016-15730	Sequence 15730, A

C 679	18	2.9	567	25	US-09-654-617-117624	Sequence 117624, A
C 680	18	2.9	567	25	US-09-654-617-197203	Sequence 197203, A
C 681	18	2.9	567	27	US-09-684-016-117624	Sequence 117624, A
C 682	18	2.9	567	27	US-09-684-016-197203	Sequence 197203, A
C 683	18	2.9	571	38	US-10-029-386-1442	Sequence 1442, Ap
C 684	18	2.9	572	21	US-09-540-228-110930	Sequence 110930, A
C 685	18	2.9	575	24	US-09-634-306B-223993	Sequence 223993, A
C 686	18	2.9	575	38	US-10-027-632-223993	Sequence 223993, A
C 687	18	2.9	575	66	US-60-226-328-2136	Sequence 2136, Ap
C 688	18	2.9	576	24	US-09-634-306B-228139	Sequence 228139, A
C 689	18	2.9	576	24	US-09-634-306B-228140	Sequence 228140, A
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C 691	18	2.9	576	38	US-10-027-632-228139	Sequence 228139, A
C 692	18	2.9	576	38	US-10-027-632-228140	Sequence 228140, A
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C 704	18	2.9	603	24	US-09-637-890-7082	Sequence 7082, Ap
C 705	18	2.9	603	25	US-09-652-814-706	Sequence 706, App
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C 707	18	2.9	610	19	US-09-521-640-23847	Sequence 23847, A
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C 710	18	2.9	610	33	US-09-865-439A-98188	Sequence 98188, A
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C 745	18	2.9	660	25	US-09-654-617-177759	Sequence 177759, A
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C 755	18	2.9	691	25	US-09-654-617-120554	Sequence 120554, A	828	18	2.9	1501	31	US-09-815-264-17231	Sequence 17231, Ap
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C 759	18	2.9	761	19	US-09-513-966A-42242	Sequence 42242, A	832	18	2.9	1516	60	US-60-164-320-1115	Sequence 1115, Ap
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C 765	18	2.9	766	38	US-10-027-632-128814	Sequence 128814, A	838	18	2.9	1723	25	US-09-655-617-263760	Sequence 263760, A
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C 790	18	2.9	1001	41	US-10-170-097-458	Sequence 458, App	863	18	2.9	2538	40	US-10-104-706A-17	Sequence 17, App1
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C 795	18	2.9	1071	19	US-09-505-532-30838	Sequence 30838, A	868	18	2.9	2643	1	PCT-US02-03987-14635	Sequence 14635, A
C 796	18	2.9	1071	31	US-09-819-091A-30838	Sequence 30838, A	869	18	2.9	2643	38	US-10-032-555-6525	Sequence 6525, Ap
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C 801	18	2.9	1105	16	US-09-270-849B-170637	Sequence 170637, A	874	18	2.9	2682	1	PCT-US02-11260-14	Sequence 14, App1
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C 935 18 2.9 8923 39 US-10-092-399-44403  
936 18 2.9 8923 40 US-10-105-299-6460  
937 18 2.9 8996 1 PCT-US02-08123-2013  
938 18 2.9 8996 1 PCT-US02-08124-854  
939 18 2.9 8996 1 PCT-US02-08276-647  
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941 18 2.9 8996 1 PCT-US02-09785-1119  
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943 18 2.9 9568 30 US-09-764-874-11389  
944 18 2.9 9568 39 US-10-092-400-11389  
C 945 18 2.9 9777 24 US-09-620-392-39027  
C 946 18 2.9 10072 23 US-09-614-150-14230  
C 947 18 2.9 10072 63 US-60-191-637-14271  
C 948 18 2.9 10072 63 US-60-191-681-11223  
949 18 2.9 10073 60 US-60-167-217-14297  
950 18 2.9 10073 61 US-60-173-464-11601  
C 951 18 2.9 10770 1 PCT-US01-01335-515  
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C 953 18 2.9 10770 30 US-09-764-905-33993  
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962 18 2.9 11706 30 US-09-764-874-12810  
963 18 2.9 11706 39 US-10-092-400-12810  
964 18 2.9 11887 24 US-09-620-392-29173  
965 18 2.9 12141 64 US-60-207-421-7  
C 966 18 2.9 12160 68 US-60-243-860-13  
C 967 18 2.9 12275 23 US-09-614-150-21997  
C 968 18 2.9 12275 61 US-60-173-464-18063  
C 969 18 2.9 12275 63 US-60-191-637-22068  
C 970 18 2.9 12275 63 US-60-191-681-17406

Sequence 233, App  
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Sequence 14794, A  
Sequence 14872, A  
Sequence 12099, A  
Sequence 14835, A  
Sequence 11697, A  
Sequence 70, Appl  
Sequence 45972, A  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 69, Appl  
Sequence 229, App  
Sequence 13784, A  
Sequence 10508, A  
Sequence 86761, A  
Sequence 4867, Ap  
Sequence 31, Appl  
Sequence 762, App  
Sequence 762, App  
Sequence 28347, A  
Sequence 59437, A  
Sequence 21593, A  
Sequence 25849, A  
Sequence 25988, A  
Sequence 20597, A  
Sequence 49866, A  
Sequence 49235, A  
Sequence 17033, A  
Sequence 60992, A  
Sequence 42403, A  
Sequence 1714, Ap  
Sequence 1816, Ap  
Sequence 42403, A  
Sequence 1266, Ap  
Sequence 4460, Ap  
Sequence 2013, Ap  
Sequence 854, App  
Sequence 647, App  
Sequence 1133, Ap  
Sequence 1139, Ap  
Sequence 11389, A  
Sequence 11389, A  
Sequence 11389, A  
Sequence 39027, A  
Sequence 14230, A  
Sequence 14271, A  
Sequence 11223, A  
Sequence 14297, A  
Sequence 11601, A  
Sequence 515, App  
Sequence 33993, A  
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Sequence 33993, A  
Sequence 23270, A  
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Sequence 1096, Ap  
Sequence 1096, Ap  
Sequence 1096, Ap  
Sequence 12810, A  
Sequence 12810, A  
Sequence 29173, A  
Sequence 7, Appl  
Sequence 13, Appl  
Sequence 21997, A  
Sequence 18063, A  
Sequence 22068, A  
Sequence 17406, A

C 971 18 2.9 12278 60 US-60-167-245-781  
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C 973 18 2.9 12613 1 PCT-US01-01354-33990  
C 974 18 2.9 12613 30 US-09-764-905-33990  
C 975 18 2.9 12613 39 US-10-074-024-514  
C 976 18 2.9 12613 39 US-10-092-399-33990  
C 977 18 2.9 12943 24 US-09-620-392-51698  
C 978 18 2.9 13216 1 PCT-US01-01354-27904  
979 18 2.9 13216 1 PCT-US01-01354-42373  
980 18 2.9 13216 1 PCT-US02-09188-1706  
981 18 2.9 13216 1 PCT-US02-09370-1808  
982 18 2.9 13216 30 US-09-764-905-27904  
983 18 2.9 13216 30 US-09-764-905-42373  
984 18 2.9 13216 36 US-10-092-399-1258  
985 18 2.9 13216 39 US-10-092-399-27904  
986 18 2.9 13216 39 US-10-092-399-42373  
987 18 2.9 13216 40 US-10-105-299-6452  
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993 18 2.9 13473 31 US-09-815-264-61535  
994 18 2.9 13623 24 US-09-620-392-3958  
995 18 2.9 13703 28 US-09-702-134-21507  
996 18 2.9 13703 31 US-09-815-264-69384  
997 18 2.9 13765 24 US-09-620-392-28845  
C 998 18 2.9 15020 24 US-09-620-392-4659  
999 18 2.9 15196 1 PCT-US01-01354-27915  
1000 18 2.9 15196 1 PCT-US01-01354-42360

## ALIGNMENTS

US-09-669-817A-33201  
; Sequence 33201, Application US/09669817A  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Ruan, Yijun G.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(5146)B  
; CURRENT APPLICATION NUMBER: US/09/669,817A  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/156,951  
; NUMBER OF SEQ ID NOS: 43701  
; SEQ ID NO 33201  
; LENGTH: 409  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: uc-osf1M202036f08b1  
US-09-669-817A-33201  
Query Match 6.4%; Score 39; DB 26; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.8e-08;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 576 AGTTTGAGGGGATTGAGACACTGTGGCTGCGCA 614  
DB 282 AGTTTGAGGGGATTGAGACACTGTGCTGCGCA 320  
RESULT 2  
US-09-654-617-406307  
; Sequence 406307, Application US/09654617  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jindong



```

; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 406307
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Oryza sativa nippohare
US-09-654-617-406307

Query Match
Best Local Similarity 100.0%; Score 39; DB 25; Length 526;
Pred. No. 1.8e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 614
DB 320 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 358

RESULT 3
US-09-684-016-406307
; Sequence 406307, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 406307
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Oryza sativa nippohare
US-09-684-016-406307

Query Match
Best Local Similarity 100.0%; Score 39; DB 27; Length 526;
Pred. No. 1.8e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 614
DB 320 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 358

RESULT 4
US-60-197-872-55012
; Sequence 55012, Application US/60197872
; GENERAL INFORMATION:
; APPLICANT: Bougri, Olegs
; APPLICANT: Byrum, Joseph R.
; APPLICANT: De La Pena, Robert C.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Shukla, Hridayabhiraanjan
; TITLE OF INVENTION: Nucleic acid Molecules and Other molecules associated with
; FILE REFERENCE: 38-21(51892)A
; CURRENT APPLICATION NUMBER: US/60/197,872
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 76255
; SEQ ID NO 55012
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Oryza sativa nippohare
; OTHER INFORMATION: Clone ID: LIB3479-005-Q6-K1-F8
US-60-197-872-55012

Query Match
Best Local Similarity 100.0%; Score 39; DB 63; Length 526;
Pred. No. 1.8e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 576 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 614
DB 320 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 358

RESULT 5
US-09-609-521-15/c
; Sequence 15, Application US/09609521
; GENERAL INFORMATION:
; APPLICANT: Unes, Scott
; TITLE OF INVENTION: PCR Selected fungal infection response
; FILE REFERENCE: 2005US
; CURRENT APPLICATION NUMBER: US/09/609,521
; CURRENT FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Rice
US-09-609-521-15

Query Match
Best Local Similarity 100.0%; Score 39; DB 23; Length 558;
Pred. No. 1.8e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 614
DB 412 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 374

RESULT 6
US-09-654-617-385773
; Sequence 385773, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 385773
; LENGTH: 3022
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-654-617-385773

Query Match
Best Local Similarity 100.0%; Score 39; DB 25; Length 3022;
Pred. No. 2e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 614
DB 320 AGTTTGAGAGGGGATTGAGACACTGTGGTGTGGCA 358

RESULT 7
US-09-684-016-385773
; Sequence 385773, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 385773
; LENGTH: 3022
```

```
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-684-016-385773

Query Match
Best Local Similarity 100.0%; Score 39; DB 27; Length 3022;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 576 AGTTTGTGAGGGGATTTGAGACACTGTGGTGTGGCA 614
DB 320 AGTTTGTGAGGGGATTTGAGACACTGTGGTGTGGCA 358

RESULT 8
US-09-654-617-407653
; Sequence 407653, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 407653
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-654-617-407653

Query Match
Best Local Similarity 100.0%; Score 37; DB 25; Length 385;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGCGCCAGCGGAAGCGCCCAAGTTCATCCGCAAG 37
DB 180 CCGCGCCAGCGGAAGCGCCCAAGTTCATCCGCAAG 216

RESULT 9
US-09-669-817A-26130
; Sequence 26130, Application US/09669817A
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Wallace, C. Kevin
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51469)B
; CURRENT APPLICATION NUMBER: US/09/669,817A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/156,951
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 43701
; SEQ ID NO 26130
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: uC-osf1M202052f03b1
US-09-669-817A-26130

Query Match
Best Local Similarity 100.0%; Score 37; DB 26; Length 385;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGCGCCAGCGGAAGCGCCCAAGTTCATCCGCAAG 37
DB 180 CCGCGCCAGCGGAAGCGCCCAAGTTCATCCGCAAG 216

RESULT 10
US-09-684-016-407653

; Sequence 407653, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 407653
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-684-016-407653

Query Match
Best Local Similarity 100.0%; Score 37; DB 27; Length 385;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGCGCCAGCGGAAGCGCCCAAGTTCATCCGCAAG 37
DB 180 CCGCGCCAGCGGAAGCGCCCAAGTTCATCCGCAAG 216

RESULT 11
US-10-015-127-1052/c
; Sequence 1052, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Spingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 1052
; LENGTH: 1775
; TYPE: DNA
; ORGANISM: Spingomonas elodea
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1775)
; OTHER INFORMATION: unsure at all n locations
US-10-015-127-1052

Query Match
Best Local Similarity 100.0%; Score 24; DB 38; Length 1775;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 308 TGTGTGATGTGTGTGTGTGTGTGTGTGTG 331
DB 1563 TGTGTGATGTGTGTGTGTGTGTGTGTGTG 1540

RESULT 12
US-60-234-446-529
; Sequence 529, Application US/60234446
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL000832
; CURRENT APPLICATION NUMBER: US/60/234,446
; CURRENT FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 1797
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 529
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? LENGTH: 32768
? TYPE: DNA
? ORGANISM: HUMAN
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(32768)
? OTHER INFORMATION: n = A,T,C or G
US-60-334-446-529

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Query Match	3.9%;	Score 24;	DB 67;	Length 32768;
Best Local Similarity	100.0%;	Pred. No. 0.9;		
Matches 24;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	303	TGCTGTGTGATGTGGTGTGT	326
Db	14972	TGCTGTGTGATGTGGTGTGT	14995

RESULT 13  
US-09-304-517A-24754  
; Sequence 24754, Application US/09304517A

```

? APPLICANT: Cheikh, Nordine
? APPLICANT: Liu, Jundong
? TITLE OF INVENTION: Annotated Plant Genes
? FILE REFERENCE: 38-21(15097)B
? CURRENT APPLICATION NUMBER: US/09/304, 517A
? CURRENT FILING DATE: 1999-05-06
? NUMBER OF SEQ ID NOS: 295529
? SEQ ID NO 24754
? LENGTH: 228
? TYPE: DNA
? ORGANISM: Zea mays
? US-09-304-517A-24754

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Query Match	3.7%	Score 23;	DB 17;	Length 228;
Best Local Similarity	100.0%	Pred. No. 2.2;		
Matches	23;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

**Qy**      15 GCGCCCCAAGTTCATCCGCAAG 37  
          |||||  
**Db**      18 GCGCCCCAAGTTCATCCGCAAG 40

```

RESULT 14
US-09-371-146A-24754
: Sequence 24754, Application US/09371146A
: GENERAL INFORMATION:
: APPLICANT: Cheilkh, Nordine
: TITLE OF INVENTION: ANNOTATED PLANT GENES
: FILE REFERENCE: 38-21(15097)C
: CURRENT APPLICATION NUMBER: US/09/371,146A
: CURRENT FILING DATE: 1999-08-09
: PRIOR APPLICATION NUMBER: US 09/304,517
: PRIOR FILING DATE: 1999-05-06
: NUMBER OF SEQ. ID NOS: 294310
: SEQ. ID NO 24754
: LENGTH: 228
: TYPE: DNA
: ORGANISM: Zea mays
US-09-371-146A-24754

```

Query Match	3.7%	Score 23	DB 17	Length 228
Best Local Similarity	100.0%	Pred. No. 2.2		
Matches 23	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 15 GGGCCCCAAGTTCATCGCAAG 37  
|||  
Db 18 GGGCCCCAAGTTCATCGCAAG 40

## RESULT 15

```

US-09-985-678-24754
: Sequence 24754, Application US/09985678
: GENERAL INFORMATION:
: APPLICANT: Cheikh, Nordine
: APPLICANT: Liu, Jingdong
: TITLE OF INVENTION: Annotated Plant Genes
: FILE REFERENCE: 16517, 255/38-21(15097) F
: CURRENT APPLICATION NUMBER: US/09/985, 678
: CURRENT FILING DATE: 2001-11-05
: PRIOR APPLICATION NUMBER: US 09/304,517
: PRIOR FILING DATE: 1999-05-06
: NUMBER OF SEQ ID NOS: 295529
: SEQ ID NO 24754
: LENGTH: 228
: TYPE: DNA
: ORGANISM: Zea mays
US-09-985-678-24754

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Query Match	3.7%	Score 23;	DB 37;	Length 228;
Best Local Similarity	100.0%	Pred. No. 2.2;		
Matches 23; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY 15 GGGCCCCAAGTTCATCCGCAAG 37  
|||  
Db 18 GGGCCCCAAGTTCATCCGCAAG 40

Search completed: April 3, 2003, 13:03:17  
Job time : 2286 secs

Search completed: April 3, 2003, 13:03:17  
Job time : 2286 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 12:29:37 ; Search time 406 Seconds  
(without alignments)  
5844.021 Million cell updates/sec

Title: US-09-856-725-2

Perfect score: 614  
Sequence: 1 ccgcgcacagcggaagcgcccc.....ggacactgtgggtgcgcgca 614

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 5543508 seqs, 1932143857 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11087016

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending\_Patents\_NA\_New.\*

1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	614	100.0	614	6	US-09-856-725-2	Sequence 2, Appl1
2	540	87.9	540	6	US-09-856-725-1	Sequence 28714, A
3	3.6	758	7	US-10-369-493-28714	Sequence 42083, A	
4	21	3.4	486	6	US-10-144-771-42083	Sequence 7004, Ap
5	21	3.4	601	6	US-09-949-002-7004	Sequence 7005, Ap
6	21	3.4	601	6	US-09-949-002-7005	Sequence 26463, A
7	21	3.4	892	8	US-10-144-771-26463	Sequence 602, App
8	21	3.4	37531	6	US-09-949-002-602	Sequence 764, App
9	21	3.4	37531	6	US-09-949-002-764	Sequence 21059, A
10	19	3.1	205	9	US-60-288-292-21059	Sequence 45025, A
11	19	3.1	305	9	US-60-141-233-45025	Sequence 31393, A
12	19	3.1	365	8	US-10-144-771-31393	Sequence 26676, A
13	19	3.1	389	8	US-10-144-771-26676	Sequence 28453, A
14	19	3.1	435	6	US-09-615-606A-28453	Sequence 159075, A
15	19	3.1	489	6	US-09-912-293-159075	Sequence 167098, A
16	19	3.1	740	6	US-09-912-293-167098	Sequence 16485, A
17	19	3.1	825	8	US-10-282-122A-16485	Sequence 13014, A
18	19	3.1	1422	7	US-10-144-771-13014	Sequence 26283, A
19	19	3.1	2265	7	US-10-369-493-26283	Sequence 10343, A
20	19	3.1	2530	9	US-60-452-680-10343	Sequence 10344, A
21	19	3.1	2609	9	US-60-452-680-10344	Sequence 1669, Ap
22	19	3.1	6668	8	US-10-311-455-1669	Sequence 2036, Ap
23	19	3.1	11726	8	US-10-311-455-2036	Sequence 18453, Ap
24	19	3.1	12269	8	US-10-311-455-1383	









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C 537	17	2.8	5062	1	PCT-US02-19297-77	Sequence 77, Appl	C 610	17	2.8	9461	9	US-60-452-680-3358	Sequence 3358, Ap
C 538	17	2.8	5062	1	PCT-US02-19592-2	Sequence 2, Appl	C 611	17	2.8	9646	9	US-60-452-680-3354	Sequence 3354, Ap
C 539	17	2.8	5062	5	US-09-949-016-499	Sequence 499, App	C 612	17	2.8	9832	8	US-10-311-455-629	Sequence 629, App
C 540	17	2.8	5062	8	US-10-159-563-325	Sequence 325, App	C 613	17	2.8	10034	8	US-10-311-455-1858	Sequence 1858, Ap
C 541	17	2.8	5062	8	US-10-101-510-58	Sequence 58, Appl	C 614	17	2.8	10039	8	US-10-311-455-2015	Sequence 2015, Ap
C 542	17	2.8	5062	8	US-10-126-052A-426	Sequence 426, App	C 615	17	2.8	10045	8	US-10-311-455-2015	Sequence 2015, Ap
C 543	17	2.8	5239	8	US-10-311-455-245	Sequence 245, App	C 616	17	2.8	10066	8	US-10-342-887-1147	Sequence 1147, Ap
C 544	17	2.8	5244	1	US-10-240-454-54	Sequence 54, Appl	C 617	17	2.8	10211	6	US-10-144-779-114	Sequence 1147, Ap
C 545	17	2.8	5313	8	PCT-US02-36935-16	Sequence 16, Appl	C 618	17	2.8	10257	9	US-09-918-624B-2	Sequence 2, Appl
C 546	17	2.8	5313	8	US-10-298-122-16	Sequence 16, Appl	C 619	17	2.8	10274	6	US-09-724-676-26096	Sequence 26096, A
C 547	17	2.8	5389	6	US-09-724-676-35634	Sequence 35634, A	C 620	17	2.8	10274	6	US-10-240-965-201	Sequence 201, App
C 548	17	2.8	5389	6	US-09-724-676-35634	Sequence 35634, A	C 621	17	2.8	10281	8	US-10-240-965-201	Sequence 201, App
C 549	17	2.8	5435	9	US-60-452-680-11737	Sequence 11737, A	C 622	17	2.8	10320	5	US-09-949-016-12117	Sequence 12117, A
C 550	17	2.8	5435	9	US-60-453-135-7350	Sequence 7350, Ap	C 623	17	2.8	10321	5	US-09-949-016-16155	Sequence 16155, A
C 551	17	2.8	5449	8	US-10-311-455-1614	Sequence 1614, Ap	C 624	17	2.8	10326	8	US-10-311-455-2140	Sequence 2140, Ap
C 552	17	2.8	5470	8	US-10-342-887-1659	Sequence 1659, Ap	C 625	17	2.8	10326	8	US-60-438-000-36	Sequence 36, Appl
C 553	17	2.8	5484	6	US-09-659-671A-178	Sequence 178, App	C 626	17	2.8	10433	8	US-10-311-455-352	Sequence 352, Appl
C 554	17	2.8	5552	8	US-10-311-455-1231	Sequence 1231, Ap	C 627	17	2.8	10562	6	US-09-724-676-26095	Sequence 26095, A
C 555	17	2.8	5576	9	US-60-452-680-8054	Sequence 19483, A	C 628	17	2.8	10565	6	US-09-724-676-26095	Sequence 26095, A
C 556	17	2.8	5576	9	US-60-452-680-8054	Sequence 8054, Ap	C 629	17	2.8	10656	6	US-09-949-016-13868	Sequence 13868, A
C 557	17	2.8	5576	9	US-60-453-135-4734	Sequence 4734, Ap	C 630	17	2.8	10656	6	US-09-949-002-679	Sequence 679, App
C 558	17	2.8	5735	8	US-10-257-166-148	Sequence 148, App	C 631	17	2.8	10666	6	US-09-949-002-735	Sequence 736, App
C 559	17	2.8	5758	8	US-10-311-455-1640	Sequence 1640, Ap	C 632	17	2.8	11050	9	US-09-949-016-14815	Sequence 14815, A
C 560	17	2.8	5912	8	US-10-311-455-575	Sequence 575, App	C 633	17	2.8	11050	9	US-60-452-680-3356	Sequence 3356, Ap
C 561	17	2.8	5937	8	US-10-240-485-95	Sequence 95, Appl	C 634	17	2.8	11103	9	US-60-452-680-3036	Sequence 3036, Ap
C 562	17	2.8	5945	8	US-10-311-455-58	Sequence 58, Appl	C 635	17	2.8	11211	5	US-09-949-016-13551	Sequence 13551, A
C 563	17	2.8	5993	1	PCT-US02-37431-1	Sequence 1, Appl	C 636	17	2.8	11260	8	US-10-240-453-27	Sequence 27, Appl
C 564	17	2.8	5993	1	US-10-301-822-1	Sequence 1, Appl	C 637	17	2.8	11285	9	US-60-452-680-3359	Sequence 3359, Ap
C 565	17	2.8	6015	9	US-60-453-135-7058	Sequence 7058, Ap	C 638	17	2.8	11288	9	US-60-452-680-3037	Sequence 3037, Ap
C 566	17	2.8	6022	8	US-10-240-453-85	Sequence 85, Appl	C 639	17	2.8	11388	8	US-10-017-161-1631	Sequence 1631, Ap
C 567	17	2.8	6022	8	US-10-311-455-1045	Sequence 1045, Ap	C 640	17	2.8	11388	8	US-10-240-453-113	Sequence 113, App
C 568	17	2.8	6035	8	US-10-311-455-1498	Sequence 1498, Ap	C 641	17	2.8	11382	5	US-09-949-016-17084	Sequence 17084, A
C 569	17	2.8	6079	8	US-10-311-455-231	Sequence 231, App	C 642	17	2.8	12237	8	US-10-311-455-1358	Sequence 231, Ap
C 570	17	2.8	6101	8	US-10-311-455-1447	Sequence 1447, Ap	C 643	17	2.8	12705	8	US-10-311-455-122	Sequence 122, App
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C 573	17	2.8	6408	8	US-10-311-455-1960	Sequence 1960, Ap	C 646	17	2.8	13420	8	US-10-311-455-889	Sequence 889, App
C 574	17	2.8	6408	8	US-10-311-455-1094	Sequence 1094, Ap	C 647	17	2.8	13427	8	US-10-311-455-1899	Sequence 1899, Ap
C 575	17	2.8	6412	8	US-10-311-455-1883	Sequence 1883, Ap	C 648	17	2.8	13449	8	US-10-311-455-1358	Sequence 1358, Ap
C 576	17	2.8	6442	8	US-10-311-455-1365	Sequence 1365, Ap	C 649	17	2.8	13449	8	US-10-311-455-1358	Sequence 1358, Ap
C 577	17	2.8	6631	8	US-10-240-453-213	Sequence 213, App	C 650	17	2.8	13574	8	US-10-311-455-1250	Sequence 1250, A
C 578	17	2.8	6631	8	US-10-240-454-16	Sequence 16, Appl	C 651	17	2.8	14241	5	US-09-949-016-13869	Sequence 13869, A
C 579	17	2.8	6712	8	US-10-311-455-663	Sequence 663, Appl	C 652	17	2.8	14253	8	US-10-311-455-1467	Sequence 1467, Ap
C 580	17	2.8	6740	8	US-10-311-455-1120	Sequence 1120, Ap	C 653	17	2.8	15399	8	US-10-311-455-1487	Sequence 1487, Ap
C 581	17	2.8	6866	8	US-10-311-455-639	Sequence 639, App	C 654	17	2.8	15518	8	US-10-240-485-147	Sequence 147, App
C 582	17	2.8	6912	8	US-10-240-453-246	Sequence 246, App	C 655	17	2.8	15518	8	US-10-311-455-2145	Sequence 2145, Ap
C 583	17	2.8	6934	8	US-10-311-455-1364	Sequence 1364, Ap	C 656	17	2.8	15674	8	US-10-240-485-30	Sequence 30, Appl
C 584	17	2.8	6988	8	US-10-311-455-2413	Sequence 2413, Ap	C 657	17	2.8	15674	8	US-10-311-455-336	Sequence 336, Appl
C 585	17	2.8	7069	8	US-10-311-455-1326	Sequence 1326, Ap	C 658	17	2.8	15704	5	US-09-949-016-17201	Sequence 17201, A
C 586	17	2.8	7108	8	US-10-257-166-78	Sequence 78, Appl	C 659	17	2.8	15782	8	US-10-240-453-9	Sequence 9, Appl
C 587	17	2.8	7143	8	US-10-311-455-955	Sequence 955, App	C 660	17	2.8	15661	8	US-10-311-455-498	Sequence 498, App
C 588	17	2.8	7317	8	US-10-240-453-47	Sequence 47, Appl	C 661	17	2.8	16167	8	US-10-240-485-81	Sequence 81, Appl
C 589	17	2.8	7359	8	US-10-311-455-1835	Sequence 1835, Ap	C 662	17	2.8	16167	8	US-10-311-455-1055	Sequence 1055, Ap
C 590	17	2.8	7498	8	US-10-311-455-229	Sequence 229, App	C 663	17	2.8	16170	8	US-10-311-455-1242	Sequence 1242, Ap
C 591	17	2.8	7498	8	US-10-311-455-229	Sequence 229, App	C 664	17	2.8	16724	8	US-10-240-485-89	Sequence 89, Appl
C 592	17	2.8	7531	9	US-60-452-680-11738	Sequence 11738, A	C 665	17	2.8	16724	8	US-10-311-455-1063	Sequence 1063, Ap
C 593	17	2.8	7531	9	US-60-452-680-11738	Sequence 11738, A	C 666	17	2.8	16724	8	US-10-311-455-1063	Sequence 1063, Ap
C 594	17	2.8	7644	8	US-10-311-455-503	Sequence 503, App	C 667	17	2.8	17203	8	US-10-311-455-1456	Sequence 1456, A
C 595	17	2.8	8131	8	US-10-240-454-22	Sequence 22, Appl	C 668	17	2.8	17419	8	US-10-240-453-111	Sequence 111, App
C 596	17	2.8	8131	8	US-10-311-455-870	Sequence 870, Appl	C 669	17	2.8	17419	8	US-10-311-455-1267	Sequence 1267, App
C 597	17	2.8	8254	8	US-10-311-455-837	Sequence 837, App	C 670	17	2.8	17721	8	US-10-311-455-1701	Sequence 1701, Ap
C 598	17	2.8	8254	8	US-10-311-455-838	Sequence 838, App	C 671	17	2.8	18512	8	US-10-311-455-950	Sequence 950, App
C 599	17	2.8	8543	8	US-10-240-453-18	Sequence 18, Appl	C 672	17	2.8	18974	5	US-09-949-016-15267	Sequence 15267, A
C 600	17	2.8	8588	8	US-10-240-453-200	Sequence 200, App	C 673	17	2.8	21537	8	US-10-311-455-1972	Sequence 1972, Ap
C 601	17	2.8	8616	9	US-60-452-680-3352	Sequence 3352, Ap	C 674	17	2.8	22143	5	US-09-949-016-15983	Sequence 15983, A
C 602	17	2.8	8616	9	US-60-452-680-3352	Sequence 3352, Ap	C 675	17	2.8	22143	5	US-09-949-016-15983	Sequence 15983, A
C 603	17	2.8	8727	9	US-60-452-680-3355	Sequence 3355, Ap	C 676	17	2.8	22865	5	US-09-947-911-8	Sequence 8, Appl
C 604	17	2.8	8801	9	US-60-452-680-3353	Sequence 3353, Ap	C 677	17	2.8	22865	5	US-09-949-016-15862	Sequence 15862, A
C 605	17	2.8	8912	9	US-60-452-680-3357	Sequence 3357, Ap	C 678	17	2.8	24314	5	US-09-949-016-15551	Sequence 15551, A
C 606	17	2.8	9087	5	US-10-257-166-48	Sequence 48, Appl	C 679	17	2.8	24396	5	US-09-949-016-11823	Sequence 11823, A
C 607	17	2.8	9160	8	US-09-949-016-15158	Sequence 15158, A	C 680	17	2.8	24497	5	US-09-949-016-14573	Sequence 14573, A
C 608	17	2.8	9160	8	US-10-311-455-1937	Sequence 1937, Ap	C 681	17	2.8	24553	5	US-09-949-016-16901	Sequence 16901, A
C 609	17	2.8	9238	8	US-10-240-453-239	Sequence 239, App	C 681	17	2.8	24553	5	US-09-949-016-16901	Sequence 16901, A



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C 829	17	2.8 111235	5	US-09-949-016-15328	Sequence 15328, A	C 902	17	2.8 527827	5	US-09-947-911-277	Sequence 277, App
830	17	2.8 112112	5	US-09-949-016-15639	Sequence 15639, A	C 903	17	2.8 529685	5	US-09-949-016-14340	Sequence 14340, A
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832	17	2.8 113604	8	US-10-227-195A-1	Sequence 2, App1	C 905	17	2.8 529885	5	US-09-949-016-14342	Sequence 14342, A
833	17	2.8 113604	8	US-10-227-195A-2	Sequence 2, App1	C 906	17	2.8 529885	5	US-09-949-016-14343	Sequence 14343, A
C 834	17	2.8 114139	5	US-09-949-016-16536	Sequence 16536, A	C 907	17	2.8 529885	5	US-09-949-016-14344	Sequence 14344, A
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839	17	2.8 122626	5	US-09-949-016-17524	Sequence 17524, A	C 912	17	2.8 540438	5	US-09-947-911-325	Sequence 325, App
C 840	17	2.8 126237	5	US-09-949-016-16674	Sequence 16674, A	C 913	17	2.8 636160	5	US-09-947-911-21	Sequence 21, App1
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842	17	2.8 129658	5	US-09-949-016-17195	Sequence 16795, A	C 915	17	2.8 656902	5	US-09-947-911-231	Sequence 231, App
843	17	2.8 129778	5	US-09-949-016-12191	Sequence 12191, A	C 916	17	2.8 659158	6	US-09-771-208A-20	Sequence 20, App1
844	17	2.8 129778	5	US-09-949-016-17075	Sequence 17075, A	C 917	17	2.8 665422	5	US-09-947-911-84	Sequence 84, App1
845	17	2.8 130085	5	US-09-947-911-360	Sequence 360, App	C 918	17	2.8 670689	5	US-09-949-016-12505	Sequence 12505, A
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C 851	17	2.8 143550	5	US-09-949-016-14143	Sequence 14143, A	C 924	17	2.8 767677	5	US-09-949-016-12147	Sequence 12147, A
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C 855	17	2.8 160759	5	US-09-949-016-16514	Sequence 16514, A	C 928	17	2.8 818128	5	US-09-949-016-14348	Sequence 14348, A
C 856	17	2.8 163032	5	US-09-949-016-16515	Sequence 16515, A	C 929	17	2.8 818128	5	US-09-949-016-14349	Sequence 14349, A
C 857	17	2.8 174259	5	US-09-949-016-11968	Sequence 11968, A	C 930	17	2.8 818128	5	US-09-949-016-14350	Sequence 14350, A
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866	17	2.8 198632	5	US-09-949-016-17393	Sequence 17393, A	C 939	17	2.8 818128	5	US-09-949-016-14359	Sequence 14359, A
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873	17	2.8 225127	5	US-09-949-016-16480	Sequence 16480, A	C 946	17	2.8 818128	5	US-09-949-016-14367	Sequence 14367, A
C 874	17	2.8 234884	5	US-09-949-016-16420	Sequence 16420, A	C 947	17	2.8 879306	5	US-09-947-911-194	Sequence 194, App
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C 877	17	2.8 241340	5	US-09-947-911-97	Sequence 97, App1	C 950	17	2.8 1037984	5	US-09-947-911-259	Sequence 259, App
879	17	2.8 247299	5	US-09-949-016-17590	Sequence 17590, A	C 951	17	2.8 1103371	6	US-09-948-124-96	Sequence 96, App1
C 880	17	2.8 253345	5	US-09-949-016-12656	Sequence 12656, A	C 952	17	2.8 1160003	5	US-09-947-911-238	Sequence 238, App
881	17	2.8 253364	5	US-09-949-016-13639	Sequence 13639, A	C 953	17	2.8 1282767	5	US-09-947-911-120	Sequence 120, App
882	17	2.8 253375	5	US-09-949-016-12849	Sequence 12849, A	C 954	17	2.8 1342585	5	US-09-947-911-152	Sequence 152, App
883	17	2.8 260286	5	US-09-949-016-17037	Sequence 17037, A	C 955	17	2.8 1342585	5	US-09-947-911-152	Sequence 152, App
884	17	2.8 260293	5	US-09-949-016-12106	Sequence 12106, A	C 956	17	2.8 1381124	5	US-09-947-911-182	Sequence 182, App
C 885	17	2.8 267482	6	US-09-949-002-659	Sequence 659, App	C 957	17	2.8 1722005	5	US-09-947-911-343	Sequence 343, App
C 886	17	2.8 267505	6	US-09-949-002-783	Sequence 783, App	C 958	17	2.8 1754382	1	PCT-US02-36123-6651	Sequence 6651, App
887	17	2.8 285966	5	US-09-949-016-12827	Sequence 12827, A	C 959	17	2.8 1974088	5	US-09-947-911-73	Sequence 73, App1
888	17	2.8 288031	5	US-09-949-016-14864	Sequence 14864, A	C 960	17	2.8 2110530	5	US-09-947-916-273	Sequence 273, App1
C 889	17	2.8 305349	5	US-09-947-911-44	Sequence 44, App1	C 961	17	2.8 2115522	5	US-09-947-911-63	Sequence 63, App1
890	17	2.8 321032	5	US-09-949-016-11852	Sequence 11852, A	C 962	17	2.8 2267436	5	US-09-947-911-230	Sequence 230, App
891	17	2.8 321032	5	US-09-949-016-14166	Sequence 14166, A	C 963	17	2.8 2277331	5	US-09-947-911-336	Sequence 336, App
C 892	17	2.8 323866	5	US-09-947-911-109	Sequence 109, App	C 964	17	2.8 2323866	6	US-09-948-124-64	Sequence 64, App1
C 893	17	2.8 360470	5	US-09-949-016-13173	Sequence 13173, A	C 965	17	2.8 242079	5	US-09-947-911-305	Sequence 305, App
894	17	2.8 390890	5	US-09-949-016-14720	Sequence 14720, A	C 966	17	2.8 2468502	5	US-09-947-911-346	Sequence 346, App
C 895	17	2.8 428116	5	US-09-947-911-220	Sequence 220, App	C 967	17	2.8 2593930	5	US-09-947-911-54	Sequence 54, App1
896	17	2.8 463588	6	US-09-948-124-58	Sequence 58, App1	C 968	17	2.8 2682138	5	US-09-947-911-255	Sequence 255, App
897	17	2.8 495619	5	US-09-947-911-55	Sequence 55, App1	C 969	17	2.8 2813043	5	US-09-947-911-103	Sequence 103, App
C 898	17	2.8 524032	5	US-09-949-016-16928	Sequence 16928, A	C 970	17	2.8 2863598	5	US-09-947-911-26	Sequence 26, App1
C 899	17	2.8 524032	5	US-09-949-016-16929	Sequence 16929, A	C 971	17	2.8 3227788	5	US-09-947-911-51	Sequence 51, App1
C 900	17	2.8 524032	5	US-09-949-016-16930	Sequence 16930, A	C 972	17	2.8 3234806	5	US-09-947-911-244	Sequence 244, App
	17	2.8 524032	5	US-09-949-016-16930	Sequence 16930, A	C 973	17	2.8 3928194	5	US-09-947-911-317	Sequence 317, App

974	1	2.8	4063095	5	US-09-947-911-323	Sequence 323, App
975	17	2.8	4604722	5	US-09-947-916-240	Sequence 240, App
976	17	2.8	4622116	5	US-09-947-916-288	Sequence 288, App
977	17	2.8	5401257	5	US-09-947-916-209	Sequence 209, App
978	17	2.8	6853926	5	US-09-947-916-137	Sequence 137, App
979	17	2.8	7928029	5	US-09-947-916-16	Sequence 16, App
980	17	2.8	8616041	5	US-09-947-916-174	Sequence 174, App
981	17	2.8	8885655	5	US-09-947-916-97	Sequence 97, App
982	16	2.6	25	5	US-09-953-570-33054	Sequence 33054, A
983	16	2.6	25	8	US-10-098-2638-B-19698	Sequence 19698, A
984	16	2.6	25	8	US-10-355-577-713277	Sequence 13277, A
985	16	2.6	25	8	US-10-355-577-30011	Sequence 30011, A
986	16	2.6	25	8	US-10-355-577-723691	Sequence 333691, A
987	16	2.6	25	9	US-10-355-577-558735	Sequence 558735, A
988	16	2.6	25	9	US-60-427-808-246244	Sequence 246244, A
989	16	2.6	25	9	US-60-427-808-832363	Sequence 832363, A
990	16	2.6	25	9	US-60-427-836-253429	Sequence 253429, A
991	16	2.6	50	6	US-09-912-293-157221	Sequence 157221, A
992	16	2.6	50	8	US-10-325-899-15261	Sequence 15261, App
993	16	2.6	51	6	US-09-912-293-42656	Sequence 42656, A
994	16	2.6	67	6	US-09-513-999C-26256	Sequence 26256, A
995	16	2.6	69	6	US-09-912-293-18393	Sequence 18393, A
996	16	2.6	81	6	US-09-513-999C-19752	Sequence 19752, A
997	16	2.6	90	6	US-09-513-999C-17489	Sequence 17489, A
998	16	2.6	92	6	US-09-513-999C-19954	Sequence 19954, A
999	16	2.6	101	8	US-10-298-192-7	Sequence 7, App
1000	16	2.6	117	6	US-09-912-293-134776	Sequence 134776, A

## ALIGNMENTS

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RESULT 1
US-09-856-725-2
; Sequence 2, Application US/09856725
; GENERAL INFORMATION:
; APPLICANT: Jun Ueki et al.
; TITLE OF INVENTION: Nucleic acid fragments, recombinant vectors containing
; TITLE OF INVENTION: the same and method for promoting expression of structural
; TITLE OF INVENTION: genes using the same.
; FILE REFERENCE: 0760-0290P
; CURRENT APPLICATION NUMBER: US/09/856,725
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-856-725-2

```

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US-09-856-725-2
RESULT 1
; Sequence 2. Application US/09856725
; GENERAL INFORMATION:
; APPLICANT: Jun UKI et al.
; TITLE OF INVENTION: Nucleic acid fragments, recombinant vectors containing
; TITLE OF INVENTION: The same and method for promoting expression of structural
; TITLE OF INVENTION: genes using the same.
; FILE REFERENCE: 0760-0290P
; CURRENT APPLICATION NUMBER: US/09/856,725
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-856-725-2

Query Match          100.0%; Score 614; DB 6; Length 614;
Best Local Similarity 100.0%; Pred. No.1.2e-305;
Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGGCGCAGGCGGAAGCGCCCCCAAGTTCATCCGCAAGGTTGGAACCTTCCTTAATCT 60
DB      1 CCGGCGCAGGCGGAAGCGCCCCCAAGTTCATCCGCAAGGTTGGAACCTTCCTTAATCT 60

QY      61 ACTGCTCTTGTGCTCTGCTCTTTTCTTTTGTGTGTCCTTTCTTGTTGTGCTTGTGATG 120
DB      61 ACTGCTCTTGTGCTCTGCTCTTTTCTTTTGTGTGTCCTTTCTTGTTGTGCTTGTGATG 120

QY      121 AGCCCGAATTGATCTGCTAGTAGGACAGTAGACAGTACAGTACAGTACAGTACAGTACAGT 180
DB      121 AGCCCGAATTGATCTGCTAGTAGGACAGTACAGTACAGTACAGTACAGTACAGTACAGT 180

QY      181 TCTGATATTATAGGAAAAAATAAGAGGTAGTAGACACAAAGATTGAGATATCTTATCA 240
DB      181 TCTGATATTATAGGAAAAAATAAGAGGTAGTAGACACAAAGATTGAGATATCTTATCA 240

QY      241 GATTGCTATTAATTAAGTCTTGCCCATTTCTTGTTTGAACCAAGTACTTTGAATCTAAG 300
DB      241 GATTGCTATTAATTAAGTCTTGCCCATTTCTTGTTTGAACCAAGTACTTTGAATCTAAG 300

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Db      361  GTTCTGCTGATGATGATGCTTGTTGTACACCAAAAATCTTGATTTGATAGGTTTAT 420
QY      458  TTATTATTAACTGACCTACTACAAATCTATTGCTGTAATGCTAATGCTGTATCACC 517
         |||||||
Db      421  TTATTATTAACTGACCTACTACAAATCTATTGCTGTAATGCTAATGCTGTATCACC 480
QY      518  TGAATGCAATGCTCTTCTTTGTTGTCTTGATCTAACGCGAGCTCAGTCAACAG 577
         |||||||
Db      481  TGAATGCAATGCTCTTCTTTGTTGTCTTGATCTAACGCGAGCTCAGTCAACAG 540

RESULT 3
US-10-369-493-28714/C
; Sequence 28714, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 28714
; LENGTH: 758
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-10-369-493-28714

Query Match      3.6%; Score 22; DB 7; Length 758;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      353  TAAAACTGAAATTTTATTATT 374
         |||||||
Db      516  TAAACTGAAATTTTATTATT 495

RESULT 4
US-10-144-771-42083
; Sequence 42083, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO: 42083
; LENGTH: 486
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-42083

Query Match      3.4%; Score 21; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      306  TGTGTGATGTGTGTGTGTGT 326
         |||||||
Db      285  TGTGTGATGTGTGTGTGTGT 305

RESULT 5
US-09-949-002-7004/C
; Sequence 7004, Application US/09949002
; GENERAL INFORMATION:

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```

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7004
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-7004

Query Match          3.4%; Score 21; DB 6; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 446 TAGAGTTTTATTATTATTATT 466
|||
Db 191 TAGAGTTTTATTATTATTATT 171

RESULT 7
US-10-144-771-26463
; Sequence 26463, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CLO01321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 26463
; LENGTH: 892
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-26463

Query Match          3.4%; Score 21; DB 8; Length 892;

```

Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 TGTGTGATGATGATGATGAT 326  
|||||  
Db 584 TGTGTGATGATGATGATGAT 604

## RESULT 8

US-09-949-002-602/c  
; Sequence 602, Application US/09949002  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/231,401  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 602  
; LENGTH: 37531  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(37531)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-002-602

Query Match 3.4%; Score 21; DB 6; Length 37531;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 446 TAGAGTTTATTTATTTATTTAT 466  
|||||  
Db 22208 TAGAGTTTATTTATTTATTTAT 22188

## RESULT 9

US-09-949-002-764/c  
; Sequence 764, Application US/09949002  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/231,401  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 764  
; LENGTH: 37531  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(37531)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-002-764

Query Match 3.4%; Score 21; DB 6; Length 37531;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 446 TAGAGTTTATTTATTTATTTAT 466  
|||||

Db 22207 TAGAGTTTATTTATTTATTTAT 22187

## RESULT 10

US-60-288-292-21059/c  
; Sequence 21059, Application US/60288292  
; GENERAL INFORMATION:  
; APPLICANT: Glenn, Matthew  
; APPLICANT: Norris, Michael G  
; TITLE OF INVENTION: Compounds isolated from forage plants  
; TITLE OF INVENTION: and methods for their use.  
; FILE REFERENCE: 1058P  
; CURRENT APPLICATION NUMBER: US/60/288,292  
; CURRENT FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 49762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21059  
; LENGTH: 205  
; TYPE: DNA  
; ORGANISM: Festuca arundinaceae  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(205)  
; OTHER INFORMATION: n = A,T,C or G  
US-60-288-292-21059

Query Match 3.1%; Score 19; DB 9; Length 205;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GACCCCTTCCTTAATCTA 61  
|||||  
Db 118 GACCCCTTCCTTAATCTA 100

## RESULT 11

US-60-141-233-45025/c  
; Sequence 45025, Application US/60141233  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15877)A  
; CURRENT APPLICATION NUMBER: US/60/141,233  
; CURRENT FILING DATE: 1999-06-29  
; NUMBER OF SEQ ID NOS: 82359  
; SEQ ID NO 45025  
; LENGTH: 305  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-60-141-233-45025

Query Match 3.1%; Score 19; DB 9; Length 305;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 TAGACAAAGATTGGAGTA 229  
|||||  
Db 294 TAGACAAAGATTGGAGTA 276

## RESULT 12

US-10-144-771-31393  
; Sequence 31393, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 31393  
; LENGTH: 365

```

; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-31393

Query Match
Best Local Similarity 3.1%; Score 19; DB 8; Length 365;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 TCCTGTGTGTGTGTGTG 418
DB 119 TCCTGTGTGTGTGTGTG 137

RESULT 13
US-10-144-771-26676
; Sequence 26676, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ. ID NOS: 47235
; SEQ. ID NO 26676
; LENGTH: 389
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-26676

Query Match
Best Local Similarity 3.1%; Score 19; DB 8; Length 389;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 TCCTGTGTGTGTGTGTG 418
DB 50 TCCTGTGTGTGTGTGTG 68

-RESULT 14
US-09-615-606A-28453
; Sequence 28453, Application US/09615606A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Coombs, Brian E.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Ia Rosa, Thomas J.
; APPLICANT: Nelson, Donald E.
; APPLICANT: Shukla, Hridayabhitrangan
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(1544)C
; CURRENT APPLICATION NUMBER: US/09/615,606A
; CURRENT FILING DATE: 2000-07-13
; NUMBER OF SEQ. ID NOS: 91663
; SEQ. ID NO 28453
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-064-Q1-K1-C11
US-09-615-606A-28453

Query Match
Best Local Similarity 3.1%; Score 19; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 GAGTTGCTGTGTGTGTG 316
DB 59 GAGTTGCTGTGTGTGTG 77

```

```

RESULT 15
US-09-912-293-159075/c
; Sequence 159075, Application US/09912293
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 100
; FILE REFERENCE: PO-100
; CURRENT APPLICATION NUMBER: US/09/912,293
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 08/103,744
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 09/249,651
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 08/104,507
; PRIOR FILING DATE: 1993-08-09
; PRIOR APPLICATION NUMBER: 08/196,363
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 09/859,490
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 08/196,362
; PRIOR FILING DATE: 1994-02-15
; PRIOR APPLICATION NUMBER: 08/221,623
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 08/220,691
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 09/741,830
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/813,155
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ. ID NOS: 24538
; SEQ. ID NO 159075
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-912-293-159075

Query Match
Best Local Similarity 3.1%; Score 19; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 CTCCTGCTCTTTTCTTTT 90
DB 340 CTCCTGCTCTTTTCTTTT 322

Search completed: April 3, 2003, 13:35:47
Job time : 512 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 10:29:18 ; Search time 2125 Seconds

(without alignments)  
8408.999 Million cell updates/sec

Title: US-09-856-725-2

Perfect score: 614  
Sequence: 1 ccgcgcacagcggagcgcgc.....ggacactctgggtctcgca 614

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_ses:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: gb\_vl:\*  
16: em\_ba:\*  
17: em\_fun:\*  
18: em\_hum:\*  
19: em\_in:\*  
20: em\_mu:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pal:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_ses:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_ocher:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_higo\_hum:\*  
40: em\_higo\_mus:\*  
41: em\_higo\_ocher:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	614	2 BD013225	BD013225 Nucleic a
2	614	100.0	614	3 BD010208	BD010208 Nucleic a
3	614	100.0	2799	6 AR005013	AR005013 Sequence
4	614	100.0	2799	6 AR037063	AR037063 Sequence
5	614	100.0	5871	8 AB001920	AB001920 Oryza sat
6	540	87.9	540	8 AP003215	AP003215 Oryza sat
7	540	87.9	540	8 BD013234	BD013234 Nucleic a
8	540	87.9	540	23 BD010207	BD010207 Nucleic a
9	9.9	135295	8	AP003282	AP003282 Oryza sat
10	39	6.4	2990	8 RICHPD2	D73411 Oryza sativ
11	39	6.4	3040	6 AR005011	AR005011 Sequence
12	39	6.4	3040	6 AR037062	AR037062 Sequence
13	39	6.4	3040	6 AR082616	AR082616 Sequence
14	25	4.1	172224	2 AC087149	AC087149 Mus muscu
15	25	4.1	190039	2 AC094071	AC094071 Rattus no
16	24	3.9	160341	9 AL161629	AL161629 Human DNA
17	24	3.9	179207	2 AC009900	AC009900 Homo sapi
18	23	3.7	2793	6 MZEPHD1	D73410 Zea mays mR
19	23	3.7	2804	6 AR005012	AR005012 Sequence
20	22	3.6	40457	2 AF039712	AF039712 Sequence
21	22	3.6	119617	2 AC121015	AC121015 Rattus no
22	22	3.6	144284	2 AC103087	AC103087 Rattus no
23	22	3.6	146602	9 CNS05TD5	AL356015 Human chr
24	22	3.6	148202	2 AC026493	AC026493 Homo sapi
25	22	3.6	150900	9 AC068075	AC068075 Homo sapi
26	22	3.6	155435	2 AC113846	AC113846 Rattus no
27	22	3.6	165713	2 AL681429	AL681429 Homo sapi
28	22	3.6	183650	9 CNS01DWA	AL136522 Human chr
29	22	3.6	190163	9 AL365402	AL365402 Human DNA
30	22	3.6	216656	10 AL731729	AL731729 Mouse DNA
31	22	3.6	226233	2 AC124520	AC124520 Mus muscu
32	22	3.6	257728	2 AC006846	AC006846 Caenorhab
33	21	3.4	305	11 AU047169	AU047169 Rattus no
34	21	3.4	488	4 AF375682	AF375682 Sus scrof
35	21	3.4	63197	2 AC020444	AC020444 Drosophil
36	21	3.4	67870	2 AC118699	AC118699 Mus muscu
37	21	3.4	68041	8 AC025814	AC025814 Arabidops
38	21	3.4	68378	2 AC113131	AC113131 Homo sapi
39	21	3.4	82529	9 AC093634	AC093634 Homo sapi
40	21	3.4	85637	9 AL391002	AL391002 Human DNA
41	21	3.4	110000	2 AC091454	Continuation (3 of
42	21	3.4	110000	2 AL672265	Continuation (5 of
43	21	3.4	126000	2 AC109739	AC109739 Rattus no
44	21	3.4	127007	10 AL627432	AL627432 Mouse DNA
45	21	3.4	130484	2 AC096109	AC096109 Rattus no
46	21	3.4	136037	9 AC004104	AC004104 Homo sapi
47	21	3.4	142811	2 AC111509	AC111509 Rattus no
48	21	3.4	146001	2 AC112747	AC112747 Rattus no
49	21	3.4	146412	2 AF130359	AF130359 Homo sapi
50	21	3.4	147003	2 AC120948	AC120948 Rattus no
51	21	3.4	147425	2 AC094576	AC094576 Rattus no
52	21	3.4	149886	3 AC149886	AF049850 Mus muscu
53	21	3.4	158405	10 MMHC310M6	AF109906 Mus muscu
54	21	3.4	159255	9 AF212831	AF212831 Homo sapi
55	21	3.4	162730	2 AC128071	AC128071 Rattus no
56	21	3.4	162737	2 AC007733	AC007733 Homo sapi
57	21	3.4	164628	9 CNS01DVU	AL155858 Human chr
58	21	3.4	167157	2 AC129272	AC129272 Rattus no
59	21	3.4	170670	2 AC117725	AC117725 Mus muscu
60	21	3.4	170670	2 AC121758	AC121758 Homo sapi
61	21	3.4	172280	2 AC098202	AC098202 Rattus no
62	21	3.4	172936	2 AC027154	AC027154 Mus muscu
63	21	3.4	173014	9 AL606500	AL606500 Human DNA
64	21	3.4	174098	2 AC115905	AC115905 Mus muscu
65	21	3.4	174503	9 AC005697	AC005697 Homo sapi

Pred. No. is the number of results predicted by chance to have a

65	21	3.4	174776	9	AL592546	Human DNA	139	20	3.3	110000	2	LMFLCHR32_20	Continuation (21
C	66	21	3.4	176221	2	AC109045	140	20	3.3	110000	2	LMFLCHR36_12	Continuation (13
68	21	3.4	176854	2	AC107796	Mus muscu	141	20	3.3	110236	2	AC116032	AC116032 Dictyost
69	21	3.4	177433	9	AC011747	Homo sapi	142	20	3.3	111264	2	AC128775	AC128775 Rattus
70	21	3.4	177720	2	AC0110452	Rattus no	143	20	3.3	111650	5	AC005215	AC005215 Homo
71	21	3.4	178975	2	AP004989	Oryza sat	144	20	3.3	113551	5	AL591213	AL591213 Zebrafis
C	72	21	3.4	179812	2	AC129999	145	20	3.3	116729	2	AC114183	AC114183 Rattus
C	73	21	3.4	180424	9	AC106860	146	20	3.3	118355	2	AC131548	AC131548 Rattus
C	74	21	3.4	181502	2	AC107850	147	20	3.3	121047	2	AC095295	AC095295 Rattus
C	75	21	3.4	183353	9	AC087071	148	20	3.3	121157	2	AC113745	AC113745 Rattus
C	76	21	3.4	184566	2	AC125590	149	20	3.3	122495	2	AC106699	AC106699 Rattus
C	77	21	3.4	186449	2	AC111954	150	20	3.3	123122	2	AC126387	AC126387 Homo
C	78	21	3.4	189236	10	AL607030	151	20	3.3	126809	2	AC124138	AC124138 Rattus
C	79	21	3.4	193589	3	AC025370	152	20	3.3	129130	2	AC130810	AC130810 Medicago
C	80	21	3.4	194335	2	AC007647	153	20	3.3	129856	9	AC016620	AC016620 Homo
C	81	21	3.4	196304	2	AC128889	154	20	3.3	129938	9	AC008071	AC008071 Homo
C	82	21	3.4	197063	2	AC129280	155	20	3.3	130391	2	AC109079	AC109079 Rattus
C	83	21	3.4	197663	2	AC011615	156	20	3.3	135109	2	AC119373	AC119373 Rattus
C	84	21	3.4	200491	9	AC007249	157	20	3.3	137353	2	AP005116	AP005116 Oryza
C	85	21	3.4	201930	2	AL840624	158	20	3.3	137557	2	AC005909	AC005909 Homo
C	86	21	3.4	204495	10	AL591884	159	20	3.3	142227	2	AL162492	AL162492 Homo
C	87	21	3.4	208804	2	AC117025	160	20	3.3	143088	9	AC005684	AC005684 Homo
C	88	21	3.4	210523	2	AL731694	161	20	3.3	144885	2	AP004819	AP004819 Oryza
C	89	21	3.4	211308	2	AC094850	162	20	3.3	145331	9	AC007877	AC007877 Homo
C	90	21	3.4	215172	2	AC126983	163	20	3.3	146310	2	AC118079	AC118079 Rattus
C	91	21	3.4	220103	2	AC073781	164	20	3.3	146437	9	AC010489	AC010489 Homo
C	92	21	3.4	224790	2	AL806523	165	20	3.3	147758	2	AC110343	AC110343 Rattus
C	93	21	3.4	225795	3	AE003713	166	20	3.3	149042	2	AC110128	AC110128 Rattus
C	94	21	3.4	227363	2	AL592002	167	20	3.3	149271	2	AC112489	AC112489 Homo
C	95	21	3.4	230085	2	AC099426	168	20	3.3	150651	2	AL157499	AL157499 Human
C	96	21	3.4	233874	2	AC094763	169	20	3.3	151243	2	AC094894	AC094894 Rattus
C	97	21	3.4	238478	10	AL663103	170	20	3.3	152053	2	AC022669	AC022669 Homo
C	98	21	3.4	294639	2	AC094709	171	20	3.3	152950	2	AC121067	AC121067 Rattus
C	99	21	3.4	340000	9	HS21C013	172	20	3.3	153602	2	AC012291	AC012291 Homo
C	100	21	3.4	347253	5	AF363578	173	20	3.3	154224	2	AC118799	AC118799 Rattus
C	101	20	3.3	3254	5	CCUAX1EX1	174	20	3.3	154645	2	AC111452	AC111452 Rattus
C	102	20	3.3	326	11	AM025073	175	20	3.3	156880	2	AC127541	AC127541 Homo
C	103	20	3.3	343	11	HSC014Y1	176	20	3.3	157190	2	AC115331	AC115331 Homo
C	104	20	3.3	390	9	HSNCX11	177	20	3.3	159413	3	AC007815	AC007815 Drosophi
C	105	20	3.3	511	11	G10355	178	20	3.3	160262	9	AC005242	AC005242 Homo
C	106	20	3.3	1332	9	HSNA42056	179	20	3.3	160562	2	AC098172	AC098172 Rattus
C	107	20	3.3	2122	9	HSN800558	180	20	3.3	162062	2	AC111445	AC111445 Rattus
C	108	20	3.3	2960	3	AY007239	181	20	3.3	163137	2	AC095946	AC095946 Rattus
C	109	20	3.3	2982	6	AX195189	182	20	3.3	163443	2	AC006280	AC006280 Plasmodi
C	110	20	3.3	5282	9	HSY13034	183	20	3.3	163783	2	AC127837	AC127837 Rattus
C	111	20	3.3	8594	9	AC106048	184	20	3.3	163935	2	AC121751	AC121751 Rattus
C	112	20	3.3	10048	6	AX458499	185	20	3.3	164490	2	AC102712	AC102712 Mus
C	113	20	3.3	11429	3	AE0012926	186	20	3.3	164958	2	AC092729	AC092729 Canis
C	114	20	3.3	12029	3	AE001408	187	20	3.3	166543	3	AC128985	AC128985 Rattus
C	115	20	3.3	12593	3	AE001418	188	20	3.3	167029	8	AP002540	AP002540 Oryza
C	116	20	3.3	37581	3	US3155	189	20	3.3	167136	2	AC110392	AC110392 Rattus
C	117	20	3.3	40940	3	CEDD2013	190	20	3.3	167863	2	AL1590651	AL1590651 Homo
C	118	20	3.3	55870	8	AC005819	191	20	3.3	168926	2	AC128358	AC128358 Rattus
C	119	20	3.3	57476	2	AC107630	192	20	3.3	169101	2	AC115732	AC115732 Mus
C	120	20	3.3	60152	2	AC126388	193	20	3.3	169427	2	AC107339	AC107339 Rattus
C	121	20	3.3	61494	2	AC118295	194	20	3.3	169687	2	AC113502	AC113502 Mus
C	122	20	3.3	61634	8	AB008269	195	20	3.3	169867	2	AC094703	AC094703 Rattus
C	123	20	3.3	66227	2	AC026534	196	20	3.3	170553	2	AC105548	AC105548 Rattus
C	124	20	3.3	70310	2	AC016436	197	20	3.3	170823	2	AC092294	AC092294 Rattus
C	125	20	3.3	71203	9	AL160251	198	20	3.3	171151	2	AC120561	AC120561 Homo
C	126	20	3.3	84107	9	HS248E1	199	20	3.3	171517	9	AC093862	AC093862 Homo
C	127	20	3.3	84825	8	AC006418	200	20	3.3	172195	2	AC0811267	AC0811267 Rattus
C	128	20	3.3	88003	2	AC0211919	201	20	3.3	172917	3	AC008142	AC008142 Homo
C	129	20	3.3	89248	2	AC001919	202	20	3.3	175917	2	AC095835	AC095835 Rattus
C	130	20	3.3	94091	8	ATF28A23	203	20	3.3	175933	2	AC094704	AC094704 Rattus
C	131	20	3.3	95234	9	AC120305	204	20	3.3	176019	2	AC0945708	AC0945708 Homo
C	132	20	3.3	95304	9	AC108163	205	20	3.3	176354	2	AC111568	AC111568 Rattus
C	133	20	3.3	96183	9	AL161896	206	20	3.3	177263	2	AC113681	AC113681 Rattus
C	134	20	3.3	97464	2	AC095194	207	20	3.3	177327	9	AC097510	AC097510 Homo
C	135	20	3.3	97614	2	AC096521	208	20	3.3	177467	2	AC023311	AC023311 Homo
C	136	20	3.3	106291	2	AC129808	209	20	3.3	178064	2	AC099516	AC099516 Homo
C	137	20	3.3	106664	10	AF130357	210	20	3.3	178157	2	AC130436	AC130436 Homo
C	138	20	3.3	106729	9	AC005320	211	20	3.3	179022	2	AC120924	AC120924 Rattus

212	20	3.3	180109	2	AC125916	AC125916 Rattus no	285	19	3.1	17419	6	AX346196	AX346196 Sequence
213	20	3.3	181477	2	AC024590	AC024590 Homo sapi	286	19	3.1	21844	2	AC130395	AC130395 Rattus no
214	20	3.3	181483	2	AC115275	AC115275 Rattus no	287	19	3.1	26001	9	AC105444	AC105444 Homo sapi
215	20	3.3	182571	2	AC095873	AC095873 Rattus no	288	19	3.1	26226	9	AL136180	AL136180 Human DNA
216	20	3.3	183253	2	AC122536	AC122536 Mus muscu	289	19	3.1	28562	2	AC009103	AC009103 Homo sapi
217	20	3.3	183695	9	AC012450	AC012450 Homo sapi	290	19	3.1	30973	2	AC097974	AC097974 Rattus no
218	20	3.3	183930	2	AC105773	AC105773 Rattus no	291	19	3.1	33960	10	HAMBHC	L12104 Mesocricetu
219	20	3.3	183965	2	AC068764	AC068764 Homo sapi	292	19	3.1	35578	3	CEH12D21	CEH12D21 Human DNA
220	20	3.3	187277	2	AC115653	AC115653 Rattus no	293	19	3.1	36128	2	CEM02B4	CEM02B4 Caenorhabdi
221	20	3.3	187311	2	AC096757	AC096757 Homo sapi	294	19	3.1	36429	3	U29380	U29380 Caenorhabdi
222	20	3.3	188464	9	AC114604	AC114604 Mus muscu	295	19	3.1	38700	3	CE709A5	CE709A5 Caenorhabdi
223	20	3.3	189944	2	AC113784	AC113784 Rattus no	296	19	3.1	39299	9	AP000362	AP000362 Homo sapi
224	20	3.3	190537	2	AC010757	AC010757 Homo sapi	297	19	3.1	41625	3	AF022973	AF022973 Caenorhab
225	20	3.3	191734	2	AC016560	AC016560 Homo sapi	298	19	3.1	43084	3	HSN80H12	HSN80H12 Human DNA
226	20	3.3	192083	2	AC015901	AC015901 Homo sapi	299	19	3.1	43374	2	CEM04B2	CEM04B2 Caenorhabdi
227	20	3.3	192861	8	ATC8RIV80	ATC8RIV80 Homo sapi	300	19	3.1	43506	8	AF325198	AF325198 Triticum
228	20	3.3	193495	2	AC117043	AC117043 Rattus no	301	19	3.1	44284	2	AC013856	AC013856 Drosophil
229	20	3.3	194487	2	AL671894	AL671894 Mus muscu	302	19	3.1	44308	8	SPBC887	SPBC887 Homo sapi
230	20	3.3	194539	2	AC125739	AC125739 Rattus no	303	19	3.1	44318	3	AF036698	AF036698 Caenorhab
231	20	3.3	195481	2	AC113303	AC113303 Mus muscu	304	19	3.1	44344	2	AC068378	AC068378 Homo sapi
232	20	3.3	195481	2	AC113303	AC113303 Mus muscu	305	19	3.1	44585	9	AL139336	AL139336 Human DNA
233	20	3.3	199134	2	AC023458	AC023458 Homo sapi	306	19	3.1	44585	2	AL139336	AL139336 Human DNA
234	20	3.3	200822	9	AL591806	AL591806 Human DNA	307	19	3.1	49904	2	AC125962	AC125962 Rattus no
235	20	3.3	200823	2	AC102989	AC102989 Rattus no	308	19	3.1	52183	2	AC113053	AC113053 Mus muscu
236	20	3.3	204570	2	AC113498	AC113498 Mus muscu	309	19	3.1	52183	2	AC119158	AC119158 Mus muscu
237	20	3.3	205656	2	AC118009	AC118009 Mus muscu	310	19	3.1	57077	2	AC131254	AC131254 Homo sapi
238	20	3.3	205993	2	AC126285	AC126285 Rattus no	311	19	3.1	58210	2	AC131254	AC131254 Homo sapi
239	20	3.3	206177	9	AC008072	AC008072 Homo sapi	312	19	3.1	59496	2	AC115843	AC115843 Mus muscu
240	20	3.3	207197	2	AC124480	AC124480 Mus muscu	313	19	3.1	60385	9	AC009511	AC009511 Homo sapi
241	20	3.3	21265	2	AC120520	AC120520 Canis fam	314	19	3.1	61912	2	AC124232	AC124232 Homo sapi
242	20	3.3	214025	9	AC007882	AC007882 Homo sapi	315	19	3.1	62615	8	CEY54E2A	CEY54E2A Caenorhab
243	20	3.3	216438	2	AC096318	AC096318 Rattus no	316	19	3.1	63604	8	AP000381	AP000381 Arabidops
244	20	3.3	222831	2	AC127033	AC127033 Homo sapi	317	19	3.1	64071	2	AC084122	AC084122 Homo sapi
245	20	3.3	224092	2	AC093940	AC093940 Rattus no	318	19	3.1	64071	2	AC084122	AC084122 Homo sapi
246	20	3.3	224870	2	AC125320	AC125320 Mus muscu	319	19	3.1	64244	2	AC122122	AC122122 Mus muscu
247	20	3.3	227856	2	AC007908	AC007908 Homo sapi	320	19	3.1	66070	2	AC119239	AC119239 Mus muscu
248	20	3.3	228094	2	AC124736	AC124736 Mus muscu	321	19	3.1	67665	2	AC101324	AC101324 Mus muscu
249	20	3.3	229144	9	AC127288	AC127288 Mus muscu	322	19	3.1	68080	2	AC116955	AC116955 Dictyoste
250	20	3.3	234542	2	HUAC002041	AC002041 Human Chr	323	19	3.1	68171	9	AL158205	AL158205 Human DNA
251	20	3.3	235302	2	AC073784	AC073784 Mus muscu	324	19	3.1	69368	2	AC101500	AC101500 Mus muscu
252	20	3.3	239861	2	AC094785	AC094785 Rattus no	325	19	3.1	70841	2	AC004287	AC004287 Drosophil
253	20	3.3	242647	3	AE003727	AE003727 Drosophil	326	19	3.1	70997	3	AC101386	AC101386 Mus muscu
254	20	3.3	244717	2	AC094351	AC094351 Rattus no	327	19	3.1	72123	2	AC103643	AC103643 Mus muscu
255	20	3.3	268775	2	AC126266	AC126266 Mus muscu	328	19	3.1	72179	2	AC096066	AC096066 Rattus no
256	20	3.3	332152	2	AL807394	AL807394 Mus muscu	329	19	3.1	73635	2	AC100991	AC100991 Mus muscu
257	20	3.3	343732	2	AC124464	AC124464 Mus muscu	330	19	3.1	73986	2	AC124000	AC124000 Homo sapi
258	19	3.1	311	11	AU047772	AU047772 Rattus no	331	19	3.1	77164	9	AL133514	AL133514 Human DNA
259	19	3.1	514	3	NCA228560	AJ228560 Neotectali	332	19	3.1	77555	9	AL359738	AL359738 Human DNA
260	19	3.1	794	6	AX099426	AX099426 Sequence	333	19	3.1	80017	2	AC016368	AC016368 Human DNA
261	19	3.1	912	6	AX055170	AX055170 Sequence	334	19	3.1	83550	9	AL390918	AL390918 Human DNA
262	19	3.1	921	6	AX055300	AX055300 Sequence	335	19	3.1	84432	8	AC005850	AC005850 Arabidops
263	19	3.1	1476	9	BC028682	BC028682 Homo sapi	336	19	3.1	86827	3	PFMAL3P5	PFMAL3P5 Plasmodiu
264	19	3.1	1517	8	AY064142	AY064142 Arabidops	337	19	3.1	88176	2	AL390202_09	AL390202_09 Continuation (10 o
265	19	3.1	1627	9	AK093152	AK093152 Homo sapi	338	19	3.1	89104	9	AL357509	AL357509 Human DNA
266	19	3.1	1820	6	AK001950	AK001950 Homo sapi	339	19	3.1	89207	2	AC124098	AC124098 Mus muscu
267	19	3.1	2554	6	AX301211	AX301211 Sequence	340	19	3.1	89811	8	AC018849	AC018849 Arabidops
268	19	3.1	3289	8	CS1012550	AJ012550 Citrus si	341	19	3.1	90571	2	AC106557	AC106557 Rattus no
269	19	3.1	3641	2	AC014885	AC014885 Drosophil	342	19	3.1	92464	5	AL606705	AL606705 Zebrafish
270	19	3.1	6179	6	AX251098	AX251098 Sequence	343	19	3.1	92611	9	AC006398	AC006398 Homo sapi
271	19	3.1	6179	6	AX344247	AX344247 Sequence	344	19	3.1	93173	2	AC094918	AC094918 Rattus no
272	19	3.1	6668	6	AX346598	AX346598 Sequence	345	19	3.1	93265	10	AP002736	AP002736 Mus muscu
273	19	3.1	7339	14	ECHPICORN	LO2971 Echovirus 2	346	19	3.1	93544	2	AC111617	AC111617 Rattus no
274	19	3.1	7339	14	S45208	S45208 polyprotein	347	19	3.1	93588	2	AC017187	AC017187 Drosophil
275	19	3.1	8325	10	AF108133	AF108133 Mus muscu	348	19	3.1	95432	8	ATT9E8	ATT9E8 Arabidops
276	19	3.1	10700	1	AE000645	AE000645 Helicobac	349	19	3.1	96079	9	HS717L17	HS717L17 Human DNA
277	19	3.1	11145	1	AE010606	AE010606 Fusobacte	350	19	3.1	98291	9	AC073538	AC073538 Homo sapi
278	19	3.1	11726	6	AX346965	AX346965 Sequence	351	19	3.1	98775	2	AC121723	AC121723 Rattus no
279	19	3.1	12269	6	AX251225	AX251225 Sequence	352	19	3.1	99036	2	AL672053	AL672053 Dictyoste
280	19	3.1	13269	6	AX346312	AX346312 Sequence	353	19	3.1	100029	10	AE014180_3	AE014180_3 Continuation (4 of
281	19	3.1	13120	3	AF016431	AF016431 Caenorhab	354	19	3.1	100132	9	AC092177	AC092177 Homo sapi
282	19	3.1	14514	2	AC115610	AC115610 Dictyoste	355	19	3.1	101567	2	AL845510	AL845510 Danio rer
283	19	3.1	17419	6	AX277936	AX277936 Sequence	356	19	3.1	102992	2	AL591863	AL591863 Homo sapi
284	19	3.1	17419	6	AX323623	AX323623 Sequence	357	19	3.1	103463	2	AC121378	AC121378 Rattus no

C 358	19	3.1 106277	9	AC068792	AC068792 Homo sapi	C 431	19	3.1 151447	3	AC010122	AC010122 Drosophila
C 359	19	3.1 106977	9	HS9E21	AL008633 Human DNA	C 432	19	3.1 151605	2	AC011995	AC011995 Homo sapi
C 360	19	3.1 107243	10	AL663097	AL663097 Mouse DNA	C 433	19	3.1 151705	2	AC117900	AC117900 Rattus no
C 361	19	3.1 107706	9	AC064856	AC064856 Homo sapi	C 434	19	3.1 152106	2	AC123198	AC123198 Rattus no
C 362	19	3.1 110000	2	AC084053	Continuation (4 of	C 435	19	3.1 152304	2	AC023032	AC023032 Homo sapi
C 363	19	3.1 110000	2	AC11891-2	Continuation (3 of	C 436	19	3.1 152831	2	AC021743	AC021743 Homo sapi
C 364	19	3.1 110000	2	AC117408-0	Continuation (6 of	C 437	19	3.1 152928	2	AC111475	AC111475 Rattus no
C 365	19	3.1 110000	2	CEY11B2-5	Continuation (20 o	C 438	19	3.1 153004	2	AC096754	AC096754 Homo sapi
C 366	19	3.1 110000	2	TMFLCHR3-19	Continuation (20 o	C 439	19	3.1 153169	2	AP001092	AP001092 Homo sapi
C 367	19	3.1 110307	9	AC116628	AC116628 Homo sapi	C 440	19	3.1 153270	2	AC091661	AC091661 Homo sapi
C 368	19	3.1 111254	9	AC125491	AC125491 Homo sapi	C 441	19	3.1 153402	2	AC006278	AC006278 Homo sapi
C 369	19	3.1 111434	5	AL591144	AL591144 Zebrafish	C 442	19	3.1 153477	2	AC024615	AC024615 Homo sapi
C 370	19	3.1 111768	9	AC102981	AC102981 Rattus no	C 443	19	3.1 153657	2	AL808121	AL808121 Homo sapi
C 371	19	3.1 116305	2	AC106876	AC106876 Homo sapi	C 444	19	3.1 153686	2	AC083965	AC083965 Homo sapi
C 372	19	3.1 116585	2	AC139153	AC139153 Homo sapi	C 445	19	3.1 153826	2	AC020663	AC020663 Homo sapi
C 373	19	3.1 117545	2	AC097773	AC097773 Rattus no	C 446	19	3.1 154218	2	AC020663	AC020663 Homo sapi
C 374	19	3.1 118008	2	AC079410	AC079410 Homo sapi	C 447	19	3.1 154308	2	AC125898	AC125898 Homo sapi
C 375	19	3.1 118489	9	AP000766	AP000766 Homo sapi	C 448	19	3.1 154560	2	AC110406	AC110406 Rattus no
C 376	19	3.1 119175	9	AC111001	AC111001 Homo sapi	C 449	19	3.1 154966	2	AP001387	AP001387 Homo sapi
C 377	19	3.1 119321	2	AC105533	AC105533 Rattus no	C 450	19	3.1 155031	2	AC096500	AC096500 Rattus no
C 378	19	3.1 119468	2	AC120537	AC120537 Oryza sat	C 451	19	3.1 155213	2	HSJ1031J8	HSJ1031J8 Homo sapi
C 379	19	3.1 119779	10	AL663079	AL663079 Mouse DNA	C 452	19	3.1 155461	9	AC007493	AC007493 Homo sapi
C 380	19	3.1 120044	2	AL590096	AL590096 Human DNA	C 453	19	3.1 155729	2	CNS01DMN	CNS01DMN Homo sapi
C 381	19	3.1 120745	9	AL534945	AL534945 Human DNA	C 454	19	3.1 155847	2	AC090415	AC090415 Homo sapi
C 382	19	3.1 121012	9	AL534945	AL534945 Human DNA	C 455	19	3.1 156617	2	AC126216	AC126216 Rattus no
C 383	19	3.1 121656	9	AL537860	AL537860 Human DNA	C 456	19	3.1 156817	2	AC009406	AC009406 Homo sapi
C 384	19	3.1 121656	9	AL537860	AL537860 Human DNA	C 457	19	3.1 157144	2	AC018514	AC018514 Homo sapi
C 385	19	3.1 123500	14	US3466	US3466 Cydia pomon	C 458	19	3.1 157454	2	AP001462	AP001462 Homo sapi
C 386	19	3.1 124704	2	AL837520	AL837520 Mus muscu	C 459	19	3.1 157723	2	AC120989	AC120989 Homo sapi
C 387	19	3.1 125672	2	AC111350	AC111350 Rattus no	C 460	19	3.1 157979	2	CNS05TMD	CNS05TMD Homo sapi
C 388	19	3.1 126752	2	AP252826	AP252826 Homo sapi	C 461	19	3.1 157979	2	AC090835	AC090835 Homo sapi
C 389	19	3.1 127221	2	AC126310	AC126310 Rattus no	C 462	19	3.1 158127	2	AC105394	AC105394 Homo sapi
C 390	19	3.1 127677	2	AC102945	AC102945 Homo sapi	C 463	19	3.1 158217	2	AC094685	AC094685 Rattus no
C 391	19	3.1 127811	2	AC008375	AC008375 Homo sapi	C 464	19	3.1 158472	2	AC110612	AC110612 Homo sapi
C 392	19	3.1 128622	2	AC114968	AC114968 Homo sapi	C 465	19	3.1 158914	2	AC109257	AC109257 Homo sapi
C 393	19	3.1 129130	2	AC130810	AC130810 Homo sapi	C 466	19	3.1 160270	2	AC111569	AC111569 Rattus no
C 394	19	3.1 129968	9	HS249F5	AL030810 Medicago	C 467	19	3.1 160498	2	AL805904	AL805904 Homo sapi
C 395	19	3.1 131318	2	CEY42E10	AL030810 Medicago	C 468	19	3.1 160658	2	AC127214	AC127214 Rattus no
C 396	19	3.1 132990	8	AC018848	AC018848 Caenorhabdi	C 469	19	3.1 161048	2	AL535894	AL535894 Human DNA
C 397	19	3.1 133154	9	HS249F5	AL120203 Human DNA	C 470	19	3.1 161988	2	AC112954	AC112954 Homo sapi
C 398	19	3.1 133240	2	AC120820	AC120820 Rattus no	C 471	19	3.1 162004	2	AC094793	AC094793 Homo sapi
C 399	19	3.1 133348	2	AC114322	AC114322 Homo sapi	C 472	19	3.1 162148	2	AC108412	AC108412 Homo sapi
C 400	19	3.1 133823	2	AC027021	AC027021 Homo sapi	C 473	19	3.1 162148	2	AC102495	AC102495 Homo sapi
C 401	19	3.1 133823	2	AC027021	AC027021 Homo sapi	C 474	19	3.1 162148	2	AC102495	AC102495 Homo sapi
C 402	19	3.1 134867	2	AC013788	AC013788 Homo sapi	C 475	19	3.1 162247	2	AC019845	AC019845 Homo sapi
C 403	19	3.1 134995	9	AL592156	AL592156 Human DNA	C 476	19	3.1 162301	2	AC011023	AC011023 Homo sapi
C 404	19	3.1 135209	9	HS42616	AL020997 Homo sapi	C 477	19	3.1 162340	2	AC105838	AC105838 Homo sapi
C 405	19	3.1 135209	9	HS42616	AL020997 Homo sapi	C 478	19	3.1 162340	2	AC121983	AC121983 Homo sapi
C 406	19	3.1 137506	9	AC004824	AC004824 Homo sapi	C 479	19	3.1 162361	2	AC023779	AC023779 Homo sapi
C 407	19	3.1 138376	9	AF069333	AF069333 Homo sapi	C 480	19	3.1 162732	2	CNS01DMN	CNS01DMN Homo sapi
C 408	19	3.1 138450	2	AC118531	AC118531 Rattus no	C 481	19	3.1 162782	2	AC1212418	AC1212418 Rattus no
C 409	19	3.1 138713	8	OSJN00150	AL662989 Oryza sat	C 482	19	3.1 162925	2	AC1018528	AC1018528 Homo sapi
C 410	19	3.1 139015	2	AL645743	AL645743 Dario rer	C 483	19	3.1 162925	2	AC1018528	AC1018528 Homo sapi
C 411	19	3.1 139589	2	AC114880	AC114880 Rattus no	C 484	19	3.1 163038	2	AC109159	AC109159 Homo sapi
C 412	19	3.1 140000	9	AP001791	AP001791 Homo sapi	C 485	19	3.1 163077	2	AC091621	AC091621 Homo sapi
C 413	19	3.1 140012	10	AL671905	AL671905 Mouse DNA	C 486	19	3.1 163375	2	AC027777	AC027777 Homo sapi
C 414	19	3.1 140596	2	RN75P15	AL603730 Rattus no	C 487	19	3.1 163483	2	AC122659	AC122659 Homo sapi
C 415	19	3.1 140677	9	AC005922	AC005922 Homo sapi	C 488	19	3.1 163521	2	AC122659	AC122659 Homo sapi
C 416	19	3.1 142154	2	AC114012	AC114012 Oryza sat	C 489	19	3.1 163660	2	AC108040	AC108040 Homo sapi
C 417	19	3.1 142855	2	AC120724	AC120724 Rattus no	C 490	19	3.1 163852	2	AC100745	AC100745 Homo sapi
C 418	19	3.1 142979	9	AC000029	AC000029 Homo sapi	C 491	19	3.1 164162	2	AC098083	AC098083 Rattus no
C 419	19	3.1 143405	2	AC062023	AC062023 Homo sapi	C 492	19	3.1 164499	2	AC092418	AC092418 Homo sapi
C 420	19	3.1 143512	2	AC087632	AC087632 Homo sapi	C 493	19	3.1 164735	2	AC090475	AC090475 Homo sapi
C 421	19	3.1 144107	2	AC010502	AC010502 Homo sapi	C 494	19	3.1 164764	2	AC102957	AC102957 Homo sapi
C 422	19	3.1 144858	2	AC105365	AC105365 Rattus no	C 495	19	3.1 165020	2	AC094130	AC094130 Homo sapi
C 423	19	3.1 145971	2	AC096698	AC096698 Rattus no	C 496	19	3.1 165120	2	CBY48C3A	CBY48C3A Homo sapi
C 424	19	3.1 145998	2	AL451078	AL451078 Homo sapi	C 497	19	3.1 165318	2	AC126747	AC126747 Homo sapi
C 425	19	3.1 146057	9	AC106963	AC106963 Rattus no	C 498	19	3.1 165318	2	AC126747	AC126747 Homo sapi
C 426	19	3.1 146073	9	HS141D16	AL773552 Homo sapi	C 499	19	3.1 165318	2	AC113324	AC113324 Homo sapi
C 427	19	3.1 146798	2	AC103616	AC103616 Mus muscu	C 500	19	3.1 166361	2	AC120917	AC120917 Homo sapi
C 428	19	3.1 146893	2	CNS08C9A	AL732553 Oryza sat	C 501	19	3.1 166664	2	AL441992	AL441992 Human DNA
C 429	19	3.1 147615	2	AC128052	AC128052 Rattus no	C 502	19	3.1 167718	2	AC023385	AC023385 Homo sapi
C 430	19	3.1 149630	2	AC118294	AC118294 Rattus no	C 503	19	3.1 167718	2	AC103212	AC103212 Rattus no

504	19	3.1.167758	2	AC110189	AC110189	Mus muscu	C 577	19	3.1.185097	2	AC023148	AC023148	Homo sapi
505	19	3.1.167872	2	AC129133	AC129133	Rattus no	578	19	3.1.185680	2	AC079738	AC079738	Homo sapi
506	19	3.1.168085	2	AC027687	AC027687	Homo sapi	579	19	3.1.185857	2	AC119608	AC119608	Rattus no
507	19	3.1.168384	2	AC121473	AC121473	Rattus no	C 580	19	3.1.186452	2	AC123796	AC123796	Mus muscu
508	19	3.1.168417	3	AC008187	AC008187	Drosophil	C 581	19	3.1.187561	2	AC130850	AC130850	Rattus no
509	19	3.1.168800	2	AC009467	AC009467	Homo sapi	582	19	3.1.187887	2	AC119553	AC119553	Rattus no
510	19	3.1.168843	2	AC109602	AC109602	Oryza sat	C 583	19	3.1.187965	2	AL591889	AL591889	Homo sapi
511	19	3.1.168968	2	AC106979	AC106979	Rattus no	C 584	19	3.1.187998	2	AC129063	AC129063	Rattus no
512	19	3.1.169022	2	AC073460	AC073460	Homo sapi	C 585	19	3.1.188062	9	AL162731	AL162731	Human DNA
513	19	3.1.169389	2	AC130505	AC130505	Rattus no	C 586	19	3.1.188456	2	AC091165	AC091165	Homo sapi
514	19	3.1.169540	9	AC024288	AC024288	Mus muscu	587	19	3.1.188682	2	AC124825	AC124825	Mus muscu
515	19	3.1.169646	9	AL160265	AL160265	Human DNA	588	19	3.1.188717	2	CNS01DPR	AL138478	Human chr
516	19	3.1.170114	9	AC044790	AC044790	Homo sapi	C 589	19	3.1.189120	2	AC102105	AC102105	Mus muscu
517	19	3.1.170241	2	AC120635	AC120635	Rattus no	C 590	19	3.1.189352	2	AC001967	AC001967	Homo sapi
518	19	3.1.170600	2	AC117316	AC117316	Rattus no	C 591	19	3.1.189486	2	AC008733	AC008733	Homo sapi
519	19	3.1.170970	9	AL354707	AL354707	Human DNA	592	19	3.1.189721	2	AC115669	AC115669	Rattus no
520	19	3.1.171050	9	AC112232	AC112232	Homo sapi	593	19	3.1.190065	2	AC094728	AC094728	Rattus no
521	19	3.1.171187	2	AC116960	AC116960	Dicystoste	C 594	19	3.1.190405	2	AC126568	AC126568	Rattus no
522	19	3.1.171238	2	AC111440	AC111440	Rattus no	595	19	3.1.190802	2	AL772261	AL772261	Mus muscu
523	19	3.1.171270	2	AC121430	AC121430	Rattus no	596	19	3.1.191044	2	AC115216	AC115216	Rattus no
524	19	3.1.171477	9	AC026457	AC026457	Homo sapi	597	19	3.1.191366	2	AC115351	AC115351	Rattus no
525	19	3.1.171506	2	AC120322	AC120322	Rattus no	598	19	3.1.191377	9	AC018398	AC018398	Homo sapi
526	19	3.1.171529	3	AC113225	AC113225	Rattus no	C 599	19	3.1.191893	2	AC126956	AC126956	Rattus no
527	19	3.1.171629	3	AC007691	AC007691	Drosophil	C 600	19	3.1.192389	2	AC007182	AC007182	Homo sapi
528	19	3.1.171709	2	AC120971	AC120971	Rattus no	C 601	19	3.1.192508	2	AL845369	AL845369	Danio rer
529	19	3.1.172148	2	AC073132	AC073132	Homo sapi	C 602	19	3.1.192582	5	AL732455	AL732455	Zebrafish
530	19	3.1.172164	2	AC079820	AC079820	Homo sapi	603	19	3.1.193282	2	AC123375	AC123375	Rattus no
531	19	3.1.172334	9	AC010650	AC010650	Homo sapi	C 604	19	3.1.193893	2	AL732612	AL732612	Mus muscu
532	19	3.1.172387	2	AC128718	AC128718	Rattus no	C 605	19	3.1.194246	2	AL627230	AL627230	Human DNA
533	19	3.1.173285	2	AC118963	AC118963	Rattus no	606	19	3.1.194459	2	AC104905	AC104905	Mus muscu
534	19	3.1.173357	9	AC113145	AC113145	Homo sapi	C 607	19	3.1.194630	2	AC128412	AC128412	Rattus no
535	19	3.1.173359	2	AC021536	AC021536	Homo sapi	608	19	3.1.194645	2	AC095402	AC095402	Rattus no
536	19	3.1.173418	2	AC110354	AC110354	Rattus no	609	19	3.1.194974	2	AC107787	AC107787	Mus muscu
537	19	3.1.173480	9	CNS00MR	AL079343	Human chr	610	19	3.1.195250	2	AC091313	AC091313	Mus muscu
538	19	3.1.173515	2	AC073394	AC073394	Homo sapi	C 611	19	3.1.195574	10	AC091782	AC091782	Genomic s
539	19	3.1.173659	2	AC017110	AC017110	Homo sapi	C 612	19	3.1.195623	2	AC124456	AC124456	Mus muscu
540	19	3.1.173824	10	AL611967	AL611967	Mouse DNA	613	19	3.1.196753	9	AC023826	AC023826	Homo sapi
541	19	3.1.174479	2	AC115824	AC115824	Mus muscu	614	19	3.1.197377	2	AC099374	AC099374	Rattus no
542	19	3.1.174615	2	AC021249	AC021249	Homo sapi	615	19	3.1.197505	2	AL611983	AL611983	Mus muscu
543	19	3.1.175302	2	AC020587	AC020587	Homo sapi	C 616	19	3.1.197629	2	AC129324	AC129324	Mus muscu
544	19	3.1.175382	9	AL157836	AL157836	Human DNA	C 617	19	3.1.197729	10	AL663056	AL663056	Mouse DNA
545	19	3.1.175844	2	AC124465	AC124465	Mus muscu	C 618	19	3.1.198269	2	AL844532	AL844532	Mus muscu
546	19	3.1.175876	2	AC102971	AC102971	Rattus no	C 619	19	3.1.198273	2	AC114897	AC114897	Mus muscu
547	19	3.1.175923	8	AC092388	AC092388	Oryza sat	C 620	19	3.1.198290	2	AC128704	AC128704	Mus muscu
548	19	3.1.175955	2	AC130138	AC130138	Rattus no	C 621	19	3.1.198390	3	AC091501	AC091501	Drosophil
549	19	3.1.177992	2	AC096699	AC096699	Rattus no	C 622	19	3.1.198634	8	ATCHRIV36	AL61536	Arabidops
550	19	3.1.178294	2	AC124880	AC124880	Rattus no	623	19	3.1.199859	10	AC110374	AC110374	Mus muscu
551	19	3.1.178786	2	AC099358	AC099358	Rattus no	624	19	3.1.200107	2	AC074229	AC074229	Mus muscu
552	19	3.1.178838	2	AC006414	AC006414	Drosophil	C 625	19	3.1.200125	10	AL589722	AL589722	Mouse DNA
553	19	3.1.179122	3	AC0069194	AC0069194	Homo sapi	C 626	19	3.1.200134	2	AC116138	AC116138	Mus muscu
554	19	3.1.180203	2	AC116731	AC116731	Mus muscu	627	19	3.1.201572	9	AC007298	AC007298	Homo sapi
555	19	3.1.180643	9	AC099555	AC099555	Papio cyn	C 628	19	3.1.201750	10	AC068294	AC068294	Mus muscu
556	19	3.1.180866	2	AC112124	AC112124	Rattus no	C 629	19	3.1.201981	2	AC073640	AC073640	Homo sapi
557	19	3.1.181076	2	AC117342	AC117342	Rattus no	C 630	19	3.1.202081	9	AL391987	AL391987	Human DNA
558	19	3.1.181193	2	AC022079	AC022079	Homo sapi	631	19	3.1.202785	2	AC109204	AC109204	Mus muscu
559	19	3.1.181598	2	AC094510	AC094510	Rattus no	632	19	3.1.202791	2	AC121577	AC121577	Mus muscu
560	19	3.1.181864	2	AC027460	AC027460	Homo sapi	633	19	3.1.203335	2	AC122056	AC122056	Mus muscu
561	19	3.1.182314	2	AC013670	AC013670	Homo sapi	634	19	3.1.203393	2	AC112938	AC112938	Mus muscu
562	19	3.1.182366	2	AL591926	AL591926	Human DNA	635	19	3.1.204263	2	AC102994	AC102994	Rattus no
563	19	3.1.182385	2	AC094602	AC094602	Rattus no	636	19	3.1.204317	2	AC117764	AC117764	Mus muscu
564	19	3.1.182659	2	AC120130	AC120130	Mus muscu	637	19	3.1.204521	2	AC130150	AC130150	Rattus no
565	19	3.1.182687	2	AC017065	AC017065	Homo sapi	638	19	3.1.204598	2	AC097682	AC097682	Rattus no
566	19	3.1.183149	2	AC129707	AC129707	Rattus no	C 639	19	3.1.205030	10	AL665911	AL665911	Mouse DNA
567	19	3.1.183215	2	AC091095	AC091095	Homo sapi	C 640	19	3.1.205164	2	AC101867	AC101867	Mus muscu
568	19	3.1.183301	2	AC102115	AC102115	Mus muscu	641	19	3.1.207629	10	AL645637	AL645637	Mouse DNA
569	19	3.1.183450	2	AC119322	AC119322	Rattus no	C 642	19	3.1.207683	2	AC098712	AC098712	Mus muscu
570	19	3.1.183900	2	AC110789	AC110789	Homo sapi	C 643	19	3.1.207905	10	AL672013	AL672013	Mouse DNA
571	19	3.1.184206	2	AC020593	AC020593	Homo sapi	C 644	19	3.1.208133	10	AL731714	AL731714	Mouse DNA
572	19	3.1.184245	2	AC120488	AC120488	Rattus no	645	19	3.1.209216	2	AL732480	AL732480	Mus muscu
573	19	3.1.184734	2	AC103610	AC103610	Mus muscu	C 646	19	3.1.209404	2	AC124688	AC124688	Mus muscu
574	19	3.1.184773	2	AC117203	AC117203	Mus muscu	647	19	3.1.209979	2	AC125045	AC125045	Mus muscu
575	19	3.1.184802	2	AC109014	AC109014	Rattus no	C 648	19	3.1.210105	2	AC125948	AC125948	Rattus no
576	19	3.1.184802	2	AC109014	AC109014	Rattus no	649	19	3.1.211505	2	AL356375	AL356375	Homo sapi

C 650	19	3.1	212074	2	AC107413	C 723	18	2.9	467	8	AF023767	AF023767
C 651	19	3.1	212080	2	AC091457	C 724	18	2.9	484	8	AF023767	AF023767
C 652	19	3.1	213044	9	AC096576	C 725	18	2.9	490	6	AX386662	AX386662
C 653	19	3.1	213225	2	AL772216	C 726	18	2.9	497	8	AF339705	AF339705
C 654	19	3.1	214332	2	AC128668	C 727	18	2.9	514	11	G63495	G63495
C 655	19	3.1	215411	2	AC015800	C 728	18	2.9	568	8	AF128936	AF128936
C 656	19	3.1	215451	10	AL669959	C 729	18	2.9	582	4	AF421451	AF421451
C 657	19	3.1	214260	2	AC120754	C 730	18	2.9	602	8	AF440668	AF440668
C 658	19	3.1	215467	2	AC013420	C 731	18	2.9	631	14	MVU80005	MVU80005
C 659	19	3.1	215727	2	AL358795	C 732	18	2.9	642	8	AF324706	AF324706
C 660	19	3.1	215788	9	AC007308	C 733	18	2.9	658	8	AF326885	AF326885
C 661	19	3.1	217164	2	AC094182	C 734	18	2.9	669	8	AF093034	AF093034
C 662	19	3.1	217948	2	AL732633	C 735	18	2.9	707	6	AX414216	AX414216
C 663	19	3.1	218186	9	AC083865	C 736	18	2.9	762	5	IPU25703	IPU25703
C 664	19	3.1	219229	2	AC111911	C 737	18	2.9	777	3	AY119066	AY119066
C 665	19	3.1	219783	2	AC109622	C 738	18	2.9	780	10	RNU96638	RNU96638
C 666	19	3.1	221374	10	AL604043	C 739	18	2.9	795	3	DROAPRT	DROAPRT
C 667	19	3.1	221842	2	AC108907	C 740	18	2.9	829	5	IPU25704	IPU25704
C 668	19	3.1	222658	10	AC055766	C 741	18	2.9	922	9	AB053319	AB053319
C 669	19	3.1	223350	2	AC110642	C 742	18	2.9	968	8	YSJLEUZA	YSJLEUZA
C 670	19	3.1	223376	2	AL772334	C 743	18	2.9	1035	3	DD1238019	DD1238019
C 671	19	3.1	223819	2	AC012503	C 744	18	2.9	1200	3	AF467678	AF467678
C 672	19	3.1	224299	2	AC130533	C 745	18	2.9	1202	3	AF177131	AF177131
C 673	19	3.1	224757	2	AC122913	C 746	18	2.9	1217	3	AF177129	AF177129
C 674	19	3.1	224939	3	AE003710	C 747	18	2.9	1219	3	AF177131	AF177131
C 675	19	3.1	225407	2	AC124428	C 748	18	2.9	1220	3	AF467677	AF467677
C 676	19	3.1	226060	2	AC079583	C 749	18	2.9	1233	3	AF177139	AF177139
C 677	19	3.1	226208	2	AC107712	C 750	18	2.9	1235	3	AF177137	AF177137
C 678	19	3.1	227073	10	AL513354	C 751	18	2.9	1237	3	AF177140	AF177140
C 679	19	3.1	233080	2	AC124591	C 752	18	2.9	1376	6	101659	101659
C 680	19	3.1	233234	2	AL772311	C 753	18	2.9	1403	10	NMPERSPS	NMPERSPS
C 681	19	3.1	234787	2	AC073780	C 754	18	2.9	1470	9	HSN277738	HSN277738
C 682	19	3.1	234851	2	AC116127	C 755	18	2.9	1491	9	AY060381	AY060381
C 683	19	3.1	235150	2	AC073776	C 756	18	2.9	1500	6	AX431757	AX431757
C 684	19	3.1	235395	9	AC002470	C 757	18	2.9	1509	3	LEPAJ5426	LEPAJ5426
C 685	19	3.1	238207	2	AC109146	C 758	18	2.9	1514	8	ATHEEDPA	ATHEEDPA
C 686	19	3.1	240825	6	AX087869	C 759	18	2.9	1514	8	HSN804207	HSN804207
C 687	19	3.1	241985	2	AL844217	C 760	18	2.9	1600	1	ATPERED	ATPERED
C 688	19	3.1	249487	10	MMU251788	C 761	18	2.9	1664	8	ATPERED	ATPERED
C 689	19	3.1	249487	10	MMU251835	C 762	18	2.9	1787	3	DROAPRT	DROAPRT
C 690	19	3.1	253447	2	AL732490	C 763	18	2.9	1983	8	SEU33817	SEU33817
C 691	19	3.1	256227	3	AE003827	C 764	18	2.9	2016	6	AY129492	AY129492
C 692	19	3.1	257703	3	CEY111B2A	C 765	18	2.9	2019	6	AX416558	AX416558
C 693	19	3.1	268247	2	AC127594	C 766	18	2.9	2077	9	AK000951	AK000951
C 694	19	3.1	269616	2	AC124183	C 767	18	2.9	2195	9	AF281970	AF281970
C 695	19	3.1	271179	3	AE003806	C 768	18	2.9	2219	8	AY065010	AY065010
C 696	19	3.1	274914	2	AL591964	C 769	18	2.9	2269	8	AF369915	AF369915
C 697	19	3.1	277058	2	AC016159	C 770	18	2.9	2301	9	AB048985	AB048985
C 698	19	3.1	286564	2	AC091428	C 771	18	2.9	2477	3	TCADYCI	TCADYCI
C 699	19	3.1	288763	2	AC124444	C 772	18	2.9	2643	6	AX489225	AX489225
C 700	19	3.1	289723	2	AC124692	C 773	18	2.9	2695	3	DDU06228	DDU06228
C 701	19	3.1	289723	2	AC122935	C 774	18	2.9	2810	6	E43895	E43895
C 702	19	3.1	300050	17	HSWY1A	C 775	18	2.9	2810	6	YSJLEU28	YSJLEU28
C 703	19	3.1	335026	3	AE003789	C 776	18	2.9	2977	8	HSJLEU28	HSJLEU28
C 704	19	3.1	340000	9	HS21C084	C 777	18	2.9	2979	9	HSJLEU28	HSJLEU28
C 705	19	3.1	340000	9	HS21C084	C 778	18	2.9	3017	8	YSCRP5	YSCRP5
C 706	19	3.1	349980	6	AX344556	C 779	18	2.9	3171	3	DDU68754	DDU68754
C 707	19	3.1	349980	6	AX344557	C 780	18	2.9	3171	3	AB046171	AB046171
C 708	19	3.1	349980	6	AX344557	C 781	18	2.9	3350	3	AY077632	AY077632
C 709	19	3.1	349980	6	AX344557	C 782	18	2.9	3416	8	SCYR237W	SCYR237W
C 710	18	2.9	249	11	HDMVTR4J	C 783	18	2.9	3451	8	SCYDL037C	SCYDL037C
C 711	18	2.9	265	8	AF363279	C 784	18	2.9	3584	8	SCYDL036C	SCYDL036C
C 712	18	2.9	278	8	AF182360	C 785	18	2.9	3878	9	HSJLEU28	HSJLEU28
C 713	18	2.9	317	9	HS303XD9	C 786	18	2.9	4000	3	AF482963	AF482963
C 714	18	2.9	348	8	AF384074	C 787	18	2.9	4893	10	AF097643	AF097643
C 715	18	2.9	371	8	AF384073	C 788	18	2.9	5001	6	AX281332	AX281332
C 716	18	2.9	387	8	AF384075	C 789	18	2.9	5001	6	AX347387	AX347387
C 717	18	2.9	416	8	AF384075	C 790	18	2.9	5001	6	AX349108	AX349108
C 718	18	2.9	417	8	AF384075	C 791	18	2.9	5194	8	AF260230	AF260230
C 719	18	2.9	417	8	AF384075	C 792	18	2.9	5208	6	AX345824	AX345824
C 720	18	2.9	443	3	AF292098	C 793	18	2.9	5273	6	AX345776	AX345776
C 721	18	2.9	461	8	AF231177	C 794	18	2.9	5296	6	AX346187	AX346187
C 722	18	2.9	461	8	AF231177	C 795	18	2.9	5296	6	AX346187	AX346187

796	18	2.9	5529	3	PEA7010	AL007010 Plasmodiu	869	18	2.9	17419	6	AX323624	AX323624 Sequence
797	18	2.9	5529	6	AX428966	AX428966 Sequence	870	18	2.9	17419	6	AX346197	AX346197 Sequence
798	18	2.9	5771	6	AX344664	AX344664 Sequence	871	18	2.9	17633	9	AL590711	AL590711 Human DNA
799	18	2.9	5856	6	AX345719	AX345719 Sequence	872	18	2.9	18133	6	AX345842	AX345842 Sequence
800	18	2.9	5856	6	AX348375	AX348375 Sequence	873	18	2.9	18133	6	AX348404	AX348404 Sequence
801	18	2.9	5915	11	G68152	G68152 CR10003 Dm	874	18	2.9	19311	6	AX251473	AX251473 Sequence
802	18	2.9	5928	6	AX251523	AX251523 Sequence	875	18	2.9	19988	8	AX067435	AX067435 Sequence
803	18	2.9	5928	6	AX347140	AX347140 Sequence	876	18	2.9	20160	2	AC019538	AC019538 Drosophi1
804	18	2.9	6041	6	AX348510	AX348510 Sequence	877	18	2.9	20303	3	CEP58H10	CEP58H10
805	18	2.9	6072	6	AX344933	AX344933 Sequence	878	18	2.9	20463	10	MMY09085	MMY09085
806	18	2.9	6091	6	AX458622	AX458622 Sequence	879	18	2.9	20606	8	SPBP22H7	SPBP22H7
807	18	2.9	6113	6	AX345704	AX345704 Sequence	880	18	2.9	20803	8	AP002805	AP002805 Oryza sat
808	18	2.9	6122	6	AS8932	AS8932 Sequence 1	881	18	2.9	22020	9	AF228048	AF228048 Homo sapi
809	18	2.9	6152	6	AR131271	AR131271 Sequence	882	18	2.9	22254	3	CET12G5	CET12G5
810	18	2.9	6154	6	AX251808	AX251808 Sequence	883	18	2.9	22950	3	CEP55H2	CEP55H2
811	18	2.9	6154	6	AX344196	AX344196 Sequence	884	18	2.9	23743	9	AC093143	AC093143 Homo sapi
812	18	2.9	6154	6	AX348599	AX348599 Sequence	885	18	2.9	24903	9	AF008191	AF008191 Homo sapi
813	18	2.9	6289	6	AX345931	AX345931 Sequence	886	18	2.9	25000	9	AP000650	AP000650 Homo sapi
814	18	2.9	6310	6	AX251968	AX251968 Sequence	887	18	2.9	25268	9	AL445434	AL445434 Human DNA
815	18	2.9	6310	6	AX344360	AX344360 Sequence	888	18	2.9	26000	9	AP000610	AP000610 Homo sapi
816	18	2.9	6310	6	AX348753	AX348753 Sequence	889	18	2.9	26011	9	AC103541	AC103541 Homo sapi
817	18	2.9	6381	6	AX281407	AX281407 Sequence	890	18	2.9	26400	9	AC024585	AC024585 Homo sapi
818	18	2.9	6381	6	AX345868	AX345868 Sequence	891	18	2.9	27479	9	HS43H13	HS43H13
819	18	2.9	6381	6	AX348675	AX348675 Sequence	892	18	2.9	27588	8	AF180335	AF180335 Glycine m
820	18	2.9	6541	6	AX344621	AX344621 Sequence	893	18	2.9	28771	9	AB014086	AB014086 Homo sapi
821	18	2.9	6631	6	AX323726	AX323726 Sequence	894	18	2.9	29047	3	CET05A10	CET05A10
822	18	2.9	6669	6	AX281141	AX281141 Sequence	895	18	2.9	29303	3	CER08H2	CER08H2
823	18	2.9	6669	6	AX345095	AX345095 Sequence	896	18	2.9	29482	3	CEM05B5	CEM05B5
824	18	2.9	6669	6	AX356372	AX356372 Sequence	897	18	2.9	29502	2	AC019902	AC019902
825	18	2.9	6671	3	PFAFP3	X65740 Plasmodiu	898	18	2.9	30523	2	AC115592	AC115592
826	18	2.9	6681	6	AX281262	AX281262 Sequence	899	18	2.9	30608	3	CEC48G7	CEC48G7
827	18	2.9	6681	6	AX345057	AX345057 Sequence	900	18	2.9	30961	3	CERF47B10	CERF47B10
828	18	2.9	6706	6	AF052006	AF052006 Dictyoste	901	18	2.9	31184	9	CNS07EG7	CNS07EG7
829	18	2.9	6740	6	AX346048	AX346048 Sequence	902	18	2.9	31638	10	AF259073	AF259073
830	18	2.9	6971	6	AX344653	AX344653 Sequence	903	18	2.9	32365	3	U12964	U12964
831	18	2.9	6978	8	YSCMLP	LO1992 Saccharomyc	904	18	2.9	32747	8	AL591367	AL591367 Human DNA
832	18	2.9	7165	6	AX344263	AX344263 Sequence	905	18	2.9	32940	8	AF457920	AF457920 Paxillus
833	18	2.9	7165	6	AX345653	AX345653 Sequence	906	18	2.9	32978	3	CEC09D8	CEC09D8
834	18	2.9	7165	6	AX348654	AX348654 Sequence	907	18	2.9	33274	3	CEP52B5	CEP52B5
835	18	2.9	7337	5	OMDNAPROI	X92380 O.mossambic	908	18	2.9	34548	6	AX349035	AX349035 Sequence
836	18	2.9	7384	6	AX345648	AX345648 Sequence	909	18	2.9	34548	6	AX349036	AX349036
837	18	2.9	7405	9	AC105380	AC105380 Homo sapi	910	18	2.9	34875	9	AC005329	AC005329 Homo sapi
838	18	2.9	7781	6	AX346071	AX346071 Sequence	911	18	2.9	35447	2	AC007181	AC007181 Homo sapi
839	18	2.9	7849	6	AX279998	AX279998 Sequence	912	18	2.9	35782	3	AF039711	AF039711 Caenorhab
840	18	2.9	7849	6	AX356454	AX356454 Sequence	913	18	2.9	35782	3	AF039711	AF039711 Caenorhab
841	18	2.9	8050	8	SCYKR035W	Z28370 S.cerevisia	914	18	2.9	36601	2	AC116981	AC116981
842	18	2.9	8148	6	AX416842	AX416842 Sequence	915	18	2.9	36687	8	SCCIVL37K	SCCIVL37K
843	18	2.9	8339	3	TOXDHRTS	LO8489 Toxoplasma	916	18	2.9	36776	8	SPAC4G8	SPAC4G8
844	18	2.9	8781	6	AX346589	AX346589 Sequence	917	18	2.9	37540	3	UB0443	UB0443
845	18	2.9	9007	6	AX251370	AX251370 Sequence	918	18	2.9	38013	9	HS117AB9	HS117AB9
846	18	2.9	9243	6	AX323640	AX323640 Sequence	919	18	2.9	38789	2	AC005124	AC005124
847	18	2.9	9243	6	AX344787	AX344787 Sequence	920	18	2.9	38955	3	CEZC84	CEZC84
848	18	2.9	9424	8	SDO404228	AL404228 Saccharom	921	18	2.9	39012	3	U61953	U61953
849	18	2.9	10729	9	AC115628	AC115628 Homo sapi	922	18	2.9	39608	9	AC009004	AC009004 Homo sapi
850	18	2.9	10781	9	HSUS8767	US8767 Homo sapien	923	18	2.9	39923	9	AL627082	AL627082 Human DNA
851	18	2.9	10831	1	AE002125	AE002125 Ureaplasma	924	18	2.9	40057	9	AC004188	AC004188 Homo sapi
852	18	2.9	11169	6	AX458580	AX458580 Sequence	925	18	2.9	40103	9	HUMHDAP	HUMHDAP
853	18	2.9	11337	6	AX251166	AX251166 Sequence	926	18	2.9	40638	10	AC005403	AC005403
854	18	2.9	11540	1	AE007573	AE007573 C10stricid1	927	18	2.9	40917	6	AX033911	AX033911 Sequence
855	18	2.9	11726	6	AX346965	AX346965 Sequence	928	18	2.9	41008	6	AX033912	AX033912 Sequence
856	18	2.9	12031	3	AF100660	AF100660 Caenorhab	929	18	2.9	41062	6	AC013168	AC013168 Drosophi1
857	18	2.9	12069	6	AX348317	AX348317 Sequence	930	18	2.9	41667	8	SPBC365	SPBC365
858	18	2.9	12069	3	AF100303	AF100303 Caenorhab	931	18	2.9	42223	3	CEP46G10	CEP46G10
859	18	2.9	12240	3	AE001424	AE001424 Plasmodiu	932	18	2.9	42499	2	AC084650	AC084650
860	18	2.9	12286	6	AX023557	AX023557 Sequence	933	18	2.9	42727	2	AC020319	AC020319 Drosophi1
861	18	2.9	13125	6	AX281446	AX281446 Sequence	934	18	2.9	42759	8	AB004535	AB004535 Schizosac
862	18	2.9	13125	6	AX346129	AX346129 Sequence	935	18	2.9	43305	9	AF025462	AF025462 Caenorhab
863	18	2.9	13125	6	AX348716	AX348716 Sequence	936	18	2.9	43323	9	AC114797	AC114797 Homo sapi
864	18	2.9	13658	1	AE014116	AE014116 Buchnera	937	18	2.9	43541	3	CBRG02A05	CBRG02A05
865	18	2.9	13784	6	AX348449	AX348449 Sequence	938	18	2.9	44033	5	AF322857	AF322857 Dnrio rer
866	18	2.9	14023	1	AE007841	AE007841 C10stricid1	939	18	2.9	44237	3	CER05H10	CER05H10
867	18	2.9	15820	8	SCDNACHXI	X73541 S.cerevisia	940	18	2.9	44724	2	AC115585	AC115585 Dictyoste
868	18	2.9	17419	6	AX277937	AX277937 Sequence	941	18	2.9	44798	9	HSWHC47	HSWHC47



C 942	18	2.9	45980	6	AX473125	AX473125 Sequence
943	18	2.9	47108	6	AX344506	AX344506 Sequence
944	18	2.9	47108	6	AX344507	AX344507 Sequence
C 945	18	2.9	47477	10	AF282401	AF282401 Mus muscu
C 946	18	2.9	47791	2	AC115593	AC115593 Dictyoste
C 947	18	2.9	47791	2	AC116305	AC116305 Dictyoste
C 948	18	2.9	47805	6	AX059496	AX059496 Sequence
C 949	18	2.9	47805	6	HS206C7	HS206C7 Human DNA
C 950	18	2.9	47958	2	AC091104	AC091104 Homo sapi
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C 953	18	2.9	48879	2	AC115081	AC115081 Homo sapi
C 954	18	2.9	49034	2	AC020402	AC020402 Drosophi
C 955	18	2.9	50100	2	AC017894	AC017894 Drosophi
956	18	2.9	50677	2	AC100189	AC100189 Homo sapi
957	18	2.9	50677	2	AC100189	AC100189 Homo sapi
C 958	18	2.9	51242	2	AC008793	AC008793 Homo sapi
C 959	18	2.9	51520	2	AC101109	AC101109 Mus muscu
C 960	18	2.9	51646	8	AC036106	AC036106 Arabidops
961	18	2.9	51705	9	AC092589	AC092589 Homo sapi
962	18	2.9	51705	9	AC004951	AC004951 Homo sapi
C 963	18	2.9	52139	9	AL161796	AL161796 Human DNA
C 964	18	2.9	52717	8	AB019227	AB019227 Arabidops
C 965	18	2.9	52813	9	AB010991	AB010991 Homo sapi
C 966	18	2.9	52912	2	AC130512	AC130512 Rattus no
C 967	18	2.9	52994	9	AL355354	AL355354 Human DNA
968	18	2.9	53035	2	AC015843	AC015843 Homo sapi
C 969	18	2.9	53440	2	AC117078	AC117078 Dictyoste
C 970	18	2.9	53504	2	AC027650	AC027650 Mus muscu
C 971	18	2.9	53510	2	AC095926	AC095926 Continuati
C 972	18	2.9	53949	2	AC090724	AC090724 Homo sapi
C 973	18	2.9	54215	2	AC014843	AC014843 Drosophi
C 974	18	2.9	54625	9	AL159879	AL159879 Human DNA
C 975	18	2.9	54929	2	AC099927	AC099927 Mus muscu
C 976	18	2.9	55368	2	AC105573	AC105573 Rattus no
C 977	18	2.9	55880	2	AC117775	AC117775 Mus muscu
978	18	2.9	55880	2	AC104653	AC104653 Rattus no
C 979	18	2.9	56080	2	AC093946	AC093946 Rattus no
C 980	18	2.9	56099	2	AC115598	AC115598 Dictyoste
981	18	2.9	56099	2	AC118706	AC118706 Mus muscu
C 982	18	2.9	56273	3	AB003199	AB003199 Drosophi
C 983	18	2.9	56822	2	AC020246	AC020246 Drosophi
C 984	18	2.9	57205	2	AC107995	AC107995 Homo sapi
C 985	18	2.9	57353	2	AC124318	AC124318 Homo sapi
C 986	18	2.9	57736	2	AC101344	AC101344 Mus muscu
C 987	18	2.9	58107	2	AC024407	AC024407 Homo sapi
C 988	18	2.9	58170	2	AC116282	AC116282 Homo sapi
C 989	18	2.9	58418	2	AC090130	AC090130 Homo sapi
C 990	18	2.9	58663	3	AC004300	AC004300 Drosophi
C 991	18	2.9	58828	2	AC099991	AC099991 Mus muscu
C 992	18	2.9	58864	2	HUMDABCD	HUMDABCD Human DNA
C 993	18	2.9	58864	2	AC090594	AC090594 Homo sapi
C 994	18	2.9	59159	2	AC130685	AC130685 Homo sapi
C 995	18	2.9	59297	9	CNS07EG8	CNS07EG8 Human chr
996	18	2.9	59349	2	AC094968	AC094968 Rattus no
C 997	18	2.9	59907	2	AC130689	AC130689 Homo sapi
C 998	18	2.9	60503	2	AC115766	AC115766 Mus muscu
C 999	18	2.9	60503	2	AC100324	AC100324 Mus muscu
C 1000	18	2.9	60539	2	AC100324	AC100324 Mus muscu

## ALIGNMENTS

RESULT 1  
BD013235  
LOCUS  
DEFINITION  
BD013235 614 bp DNA linear PAT 02-AUG-2002  
Nucleic acid fragment, recombinant vector containing the same and  
method of promoting the expression of structural gene by using the  
same

ACCESSION  
BD013235  
VERSION  
BD013235.1  
KEYWORDS  
WO 0123544-A/2.  
GI:22093424

SOURCE		Oryza sativa.
ORGANISM		Oryza sativa
REFERENCE		Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS		Ueki,J. and Morioka,S.
TITLE		1 (bases 1 to 614)
JOURNAL		Nucleic acid fragment, recombinant vector containing the same and Patent: WO 0123544-A 2 05-APR-2001.
COMMENT		JAPAN TOBACCO INC. JUN UEKI, SHINTI MORIOKA
OS		Oryza sativa (rice)
PN		WO 0123544-A/2
PD		05-APR-2001
PF		25-SEP-2000 WO 2000JP006560
PR		27-SEP-1999 JP 99P 271762
PI		JUN UEKI, SHINTI MORIOKA
PC		C12N15/11, C12N15/63, C12N15/82, C12N5/14, C12N9/16, A01H5/00 CC
FH		Key Location/Qualifiers
FEATURES		Location/Qualifiers
source		1..614
BASE COUNT		146 a 114 c 131 g 223 t
ORIGIN		/organism="Oryza sativa"
		/db xref="taxon:4530"
Query Match		100.0%; Score 614; DB 6; Length 614;
Best Local Similarity		100.0%; Pred. No. 6,7e-311;
Matches 614; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CCCGCGCAGCGGAGGAGCCCGCAAGTTCATCGGCAAGTTGGAGACCTTCTCTTAATCT 60
DB	1	CCCGCGCAGCGGAGGAGCCCGCAAGTTCATCGGCAAGTTGGAGACCTTCTCTTAATCT 60
QY	61	ACTCGCTTTGCTCTTCTCTTTCTTTTGTGTGCTTCTTCTTGTGTGCTTGTGCTTGTGCT 120
DB	61	ACTCGCTTTGCTCTTCTCTTTCTTTTGTGTGCTTCTTCTTGTGTGCTTGTGCTTGTGCT 120
QY	121	AGCCCGAATTTGATCGTCGTCAGTCGACGTACGATGATGATGATGATGATGATGATGAT 180
DB	121	AGCCCGAATTTGATCGTCGTCAGTCGACGTACGATGATGATGATGATGATGATGATGAT 180
QY	181	TCGTGATTAATTAAGAAATTAAGAGTAGTAGCAAGATTTGGAGATCTTCTATCA 240
DB	181	TCGTGATTAATTAAGAAATTAAGAGTAGTAGCAAGATTTGGAGATCTTCTATCA 240
QY	241	GATTCGATTAATTAAGAGTAGTAGCAAGATTTGGAGATCTTCTATCA 300
DB	241	GATTCGATTAATTAAGAGTAGTAGCAAGATTTGGAGATCTTCTATCA 300
QY	301	TTTGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB	301	TTTGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY	361	AAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB	361	AAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
QY	421	TGTGCAACCAAAATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
DB	421	TGTGCAACCAAAATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
QY	481	AAATCTATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB	481	AAATCTATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY	541	GTTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
DB	541	GTTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
QY	601	TGTGCTGTGCTGCA 614
DB	601	TGTGCTGTGCTGCA 614





[illegible]

RESULT 5	LOCUS	DEFINITION	AB001920	5871 bp	DNA	linear	PLN_05-APR-2002
AB001920		<i>Oryza sativa</i> (japonica cultivar-group) complete cds.					gene for phospholipase D <sub>1</sub>
ACCESSION	AB001920						
VERSION	AB001920.1						GI:1902902
KEYWORDS							
SOURCE		<i>Oryza sativa</i> (japonica cultivar-group) (cultivar: 'Koshihikari') leaf					

ORGANISM  
DNA.  
*Oryza sativa* (Japonica cultivar-group) (cultivar:Koshihikari) leaf  
Japonica  
*Oryza sativa* (Japonica cultivar-group)  
Euxaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;  
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzaceae; Oryza.  
1 (bases 1522 to 1665; 1839 to 1983; 2524 to 4420)  
Ueki,T., Morioka,S., Komari,T. and Kumashtiro,T.  
Purification and characterization of phospholipase D (PLD) from  
rice (*Oryza sativa* L.) and cloning of cDNA for PLD from rice and  
maize (Zea mays L.)  
Plant Cell Physiol. 36 (5), 903-914 (1995)  
96012933  
7551587  
2 (bases 1 to 5871)  
Morioka,S., Ueki,T. and Komari,T.  
Characterization of two distinctive genomic clones (Accession Nos.  
AB001919 and AB001920) for phospholipase D from rice (GRS7-076)  
Plant Physiol. 114, 396 (1997)  
3 (bases 1 to 5871)  
Ueki,T.  
Direct Submission  
Submitted (11-OCT-1995) Jun Ueki, Japan Tobacco Inc., Plant  
Breeding and Genetics Research Lab, 700 Higashihara, Iwata,  
Shizuoka 438-0802, Japan (E-mail:jun.ueki@pbgrl.jti.co.jp).  
Tel:81-538-32-7111, Fax:81-538-32-8700)  
Location:Analysar

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exon	/cultivar="Koshihikari"
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AGVRSKYRGVYTFPSOROGCKTLYODAHVDPNFIKRIPLADKNEYRHCWEDI  
PDAISAOHLITITGMSVTEITLVDSNRPKRGVGLVGLKKAASGVRLVLM  
DRTSVGLKRDGLMAHDEETENYFHGSDVNCVLCPNDDSGSIVQDLSITMFTH  
HOKIVVDELHPNQSQRRIVSFVGLGLCDGRVDTQVHSLFRITLDSITHDPHQPN  
FATASIKGSGPREPMHDHSRLBEPILAMVLYNFEQRMKOGKGLLLOLRDSDTI  
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FTYIVVPMPEBESVGSVQAILDMQRKTWMTYDITBALQAKIENAPKDYLTFF  
CIGNREKQAGEYQPEBOPADTDYSRAQEARFMYVHTKMIIVDEYIIIGSANIN  
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1984..2523  
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2524..4420  
exon  
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4421..4898  
intron  
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exon  
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BASE COUNT 1488 a 1363 c 1355 g 1665 t  
ORIGIN

Query Match 100.0%; Score 614; DB 8; Length 5871;  
Best Local Similarity 100.0%; Pred. No. 5.5e-311;  
Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCGCGCAGGGAAGCCGCCAAGTTCATCCGCAAGTTCGAGCCCTTCTCTATCT 60  
Db 1947 CCGCGCAGGGAAGCCGCCAAGTTCATCCGCAAGTTCGAGCCCTTCTCTATCT 2006  
QY 61 ACTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Db 2007 ACTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2066  
QY 121 AGCCGCAATTGATCTGCTAGTGCAGTACAGTACATACATGAAAGCATCTGGAAT 180  
Db 2067 AGCCGCAATTGATCTGCTAGTGCAGTACAGTACATACATGAAAGCATCTGGAAT 2126  
QY 181 TCTGATTTATAGGAAATTAAGAGGTAGTACAGAAATTTGAGATCTTCTATCAA 240  
Db 2127 TCTGATTTATAGGAAATTAAGAGGTAGTACAGAAATTTGAGATCTTCTATCAA 2186  
QY 241 GATTGCTCTATTAAGTGGCCATTTCTTGTGACCCCAAGTACTTCTTGAATCTAG 300  
Db 2187 GATTGCTCTATTAAGTGGCCATTTCTTGTGACCCCAAGTACTTCTTGAATCTAG 2246  
QY 301 TTGCTGTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360  
Db 2247 TTGCTGTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2306  
QY 361 AAATTTATTTATTAAGTCTCTAAATATGATGAGTCTCTGTGTGTGTGTGTGTGT 420  
Db 2307 AAATTTATTTATTAAGTCTCTAAATATGATGAGTCTCTGTGTGTGTGTGTGTGT 2366  
QY 421 TGTGTCAACAAAATCTTGATTTGATAGAGTTTATTTATTTATTAAGTCACTACTAC 480  
Db 2367 TGTGTCAACAAAATCTTGATTTGATAGAGTTTATTTATTTATTAAGTCACTACTAC 2426  
QY 481 AAATCTATTTGCTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
Db 2427 AAATCTATTTGCTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2486  
QY 541 GTTGTTCTGTATCAACAGGTGATGCAAGTTTGTGGAGGGAGTTGAGGACAC 600  
Db 2487 GTTGTTCTGTATCAACAGGTGATGCAAGTTTGTGGAGGGAGTTGAGGACAC 2546  
QY 601 TGTGGTGTGTGGCA 614

Db 2547 TGTGGTGTGTGGCA 2560  
RESULT 6  
AP003215/c  
LOCUS  
DEFINITION  
AP003215  
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,  
BAC clone:OSJNBa0089K24.  
AP003215  
GI:15128217  
AP003215.3  
Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,  
clone:OSJNBa0089K24.  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriatroidae; Oryzaceae; Oryza.  
ORGANISM  
SOURCE  
KEYWORDS  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (19-FEB-2001) Takuji Sasaki, National Institute of  
Agrobiological Resources, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasak@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
On Aug 9, 2001 this sequence version replaced gi:1342957.  
Genes were predicted from the integrated results of the following:  
GENSCAN 0. BLAST2.0. BLASTX2.0 as well as SplicePredictor  
(October 1998 version). The genomic sequence was searched against  
NCBI Nonredundant Protein database, nr  
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at  
RGP. Protein homologues of the coding regions were searched against  
NCBI Nonredundant Protein database with BLASTP2.0. ESTs represent  
the identified cDNA sequences using BLASTN 2.0 with the  
corresponding DBI accession no. and RGP clone ID.  
A gene with identity or significant homology to a protein is  
classified based on the protein name to indicate the homology level  
such as same name, 'putative-' and '-like protein'. A gene without  
significant homology to any protein but with EST homology (covering  
almost the entire length of partial sequence) is classified as an  
'unknown' protein. A gene predicted with a gene prediction program  
is classified as a 'hypothetical' protein.  
The orientation of the sequence is from -21M13 to M13Rev of the BAC  
clone. This sequence of OSJNBa0089K24 clone has an overlap with  
P0013F10 clone (DBJ: AP002523) at the position 151,639 to 154,137  
of 3' end. The sequence of this clone ends at the position 2,499 of  
P0013F10. Detailed information on overlap and assembly quality  
together with annotation of this entry is available at  
http://rgp.dna.affrc.go.jp/Genomeseg.html.  
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FEATURES

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CDS

gene  
CDS  
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probably inactive due to no termination codon in CDS  
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MNSKQDTEAKLADLEIYVSSVELSTOEBVARKVDRMAHRSHDPOPTIPVYVSPG  
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SAMILMEIQRARRRGVYDTGFIIDPRKIRKTEMIDKYEKTEDNLVHLTQOHEKTFIL  
PYNTEFFHWLFFPFDACRVYVYDSMNKEEKVDFVFOIIDRAMRPROLVGTWKEK  
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Query Match 91.7%; Score 563; DB 8; Length 154137;  
Best Local Similarity 99.8%; Pred. No. 2,4e-284;  
Matches 613; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	CCGCGCCAGCGGAAGCGCCCAAGTTATCCGCAAGTTGCGACCTTCTCCTTAATCT	60
DB	910	CCGCGCCAGCGGAAGCGCCCAAGTTATCCGCAAGTTGCGACCTTCTCCTTAATCT	851
QY	61	ACTCGCTTGTCTGCTCTTCTTCTTGTGTCCTTCTTGTGTGCGCTTGATG	120
DB	850	ACTCGCTTGTCTGCTCTTCTTCTTGTGTCCTTCTTGTGTGCGCTTGATG	791



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Query Match      87.9%; Score 540; DB 23; length 540;
Best Local Similarity 100.0%; Pred. No. 4.7e-272;
Matches 540; Conservative 0; Mismatches 0; Gaps 0
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QY	38	GTTCGGACCCCTTCCTCTTAATCTA	CTGCTGCTTGGCTGTGCTCTTTTCTTTTCTTTTGTGTGCC	97
Db	1	GTTCGGACCCCTTCCTCTTAATCTA	CTGCTGCTTGGCTGTGCTCTTTTCTTTTGTGTGCC	60
QY	98	TTTCTTGCTGTGCTTGGCTTGCATG	AGCCCGAATTTGATCTGCTAGTGCACAGTACAGTCAG	157
Db	61	TTTCTTGCTGTGCTTGGCTTGCATG	AGCCCGAATTTGATCTGCTAGTGCACAGTACAGTCAG	120
QY	158	ATACACTGAAACCATCTGGAATAAT	TGGAATTTAGAGAAAAATTAAGAGTAGTAGACA	217
Db	121	ATACACTGAAACCATCTGGAATAAT	TGGAATTTAGAGAAAAATTAAGAGTAGTAGACA	180
QY	218	GAAATGGAAGTACTTCTCTATCAAG	TTGGTCTATTAATGCTTGCCCATTTCTTGTTGACC	277
Db	181	GAAATGGAAGTACTTCTCTATCAAG	TTGGTCTATTAATGCTTGCCCATTTCTTGTTGACC	240
QY	278	CAAGTACTTCTTGAATCTAGAGTTG	CTGTGTGATGATGGAGGTGTGTGTGTGCACCA	337
Db	241	CAAGTACTTCTTGAATCTAGAGTTG	CTGTGTGATGATGGAGGTGTGTGTGTGTGCACCA	300
QY	338	AAAACTCTCATAGCTAAACCTGAAT	TTTATTTATTAATGACCTACTAAATAATGTAGA	397
Db	301	AAAACTCTCATAGCTAAACCTGAAT	TTTATTTATTAATGACCTACTAAATAATGTAGA	360
QY	398	GTTCTCTGTGTGTGATGTGTGCTTG	TGTGCACCAAAAATCTTGATTTGATAGAGTTTTAT	457
Db	361	GTTCTCTGTGTGTGATGTGTGCTTG	TGTGCACCAAAAATCTTGATTTGATAGAGTTTTAT	420
QY	458	TTATTTATTAATGACCTACTAAAC	CTATATTTGCTGTATGCTATGTGTGTGTATACAC	517
Db	421	TTATTTATTAATGACCTACTAAAC	CTATATTTGCTGTATGCTATGTGTGTGTATACAC	480
QY	518	TGAATGCAATGCTCTTCTCTTGTGT	TTCTGATCTTAACAGTGAGTCAATGTCAACAG	577
Db	481	TGAATGCAATGCTCTTCTCTTGTGT	TTCTGATCTTAACAGTGAGTCAATGTCAACAG	540

RESULT 9	AP003282/c						
LOCUS	AP003282	135295 bp	DNA	linear	PLN 21-MAR-2007		
DEFINITION	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:p05053G08.						
ACCESSION	AP003282						
VERSION	AP003282.2	GI:15004914					
KEYWORDS							
SOURCE	Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:p05053G08.						
ORGANISM	Oryza sativa (japonica cultivar-group)						
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;						
	Ehhartriodeae; Oryzaceae; Oryza.						
REFERENCE	1 Sasaki, T., Matsumoto, T. and Yamamoto, K.						
AUTHORS							

*Oryza sativa nipoonbare*(GA3) genomic DNA, chromosome 1, PAC  
 clone: P0583608  
 Published Only in Database (2001)  
 2 (bases 1 to 135295)  
 Sasaki,T., Matsumoto,T. and Yamamoto,K.  
 Direct Submission  
 Submitted (19-FEB-2001) Takuji Sasaki, National Institute of

On Jul 24, 2001 this sequence version replaced gi:13027112. Genes were predicted from the integrated results of the following: GENSCAN1.0, BLASTX2.0, BLASTY2.0 as well as SplicePredictor (October 1998 version). The gene's name was changed to *LOC130271*.

**Source**

corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein and 'like protein'. A gene without almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein. The orientation of the sequence is from 5' to 3' of the PAC clone. This sequence of P0583G08 clone has an overlap with OJ12765806 (DDBJ: AP003339) clone at the position 1 to 15,586 and with OSUNBa00895K24 (DDBJ: AP003215) at the position 134,939 to 135,295 of 5' end. The sequence of this clone starts at the position 159,588 of OJ1276606 and ends at the position 336 of OSUNBa0089K24. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://tsgp.dna.affrc.go.jp/genomeseg.html>.

**Source**

gene  
CDS

CDS

gene

CDS

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gene join(13372..13429,13884..13952,15928..16063,17127..17291,  
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22949..23016,24394..24532,24781..24889,25112..25222)  
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RLP.SADVEGNPGLCLSRCPGADSRARARARAVAVLSALVALLAAAFVLFG  
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AVYRASIPSTGVAIVAKKPRSSDEASVDNACVAGVLP.PRHHNITRILGIMANRRT  
L.PDYVLPNGTGG.LHKGGAAGCAVVENRVLSTAVGABSLALHSDVAILHR  
DYSNDNILGERTACIADFGARVADGANSNP.PPAGISYGTIAYEGMTYITKS  
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VOEMIALGIALICASTRPEDRPTKMDVAL.LGLHDDHDAEYKOKSGSIAEMADP  
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STSDHEVQSTNSPYTGELAKLALHNAVGYVDQYGAKASINWSARVATAE  
FUSQIYVWSGFNDLNTLEAGQVSPBLVGNDRPFTVTTDAVQATGCTNLCS  
GEVQTNRLAI.AAALSPTSVMNGRQFDISL.IWKDPRHWM.LQGLSGPLVGPSSL  
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54455..54502,55438..55574,56735..56928,57099..57208,  
57321..57439,57764..57842)  
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54455..54502,55438..55574,56735..56928,57099..57208,  
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NNAFEEVAVLRVITLQDKYKLFISGTVESADREVHLVIGILGNMVIYASVKEQNL  
PVMGGRKICVADDESSCAALRMASNTLRSGDMLJHNVNSIEGQAVOLMOS  
GSLPLAEPSPBHVAKTYAVSPDETTLEILNMSORVENVAKTLVGDPAKLYEA  
VDLVPNLNCIVGNRGISTLKRALMGSVSSYIYNNATCPVTYKENT"  
join(59847..60174,60209..60263,60286..60574,61172..61324,  
62306..63169,63296..63409,64875..65140,65697..65993,  
66434..66804,67702..67758,68058..68086,68430..70194,  
70984..71093,71170..71237,71444..71558)  
/gene="P0583G08.9"

Query Match 9.9%; Score 61; DB 8; Length 135295;  
Best Local Similarity 100.0%; Pred. No. 7.2e-21;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 554 TAACACGTGAGCCATCTCAACAGTTTGTGAGAGGATTGAGACACTGTGGGCTGCGC 613  
DB 135295 TAAACGCTGAGCTCATGTCAACAGTTTGTGAGAGGATTGAGACACTGTGGGCTGCGC 135236

QY 614 A 614  
DB 135235 A 135235

RESULT 10  
R1CPHD2 2990 bp mRNA linear PLN 05-APR-2002  
LOCUS Oryza sativa (japonica cultivar-group) mRNA for phospholipase D,  
DEFINITION complete cds.  
ACCESSION D73411.1 GI:1020414  
VERSION D73411  
KEYWORDS Oryza sativa (japonica cultivar-group) (cultivar:Koshihikari)  
SOURCE immature seed cDNA to mRNA.  
ORGANISM Oryza sativa (japonica cultivar-group); Embryophyta; Tracheophyta;  
Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erbartoideae; Oryzaceae; Oryza.  
REFERENCE Ueki,J., Morioka,S., Komari,T. and Kumashiro,T.  
AUTHORS Purification and characterization of phospholipase D (PLD) from  
TITLE rice (Oryza sativa L.) and cloning of cDNA for PLD from rice and  
maize (Zea mays L.)



JOURNAL Plant Cell Physiol. 36 (5), 903-914 (1995)  
 MEDLINE 96012933  
 REFERENCE 2 (bases 1 to 2990)  
 AUTHORS Ueki,J  
 JOURNAL TITLE Direct Submission  
 Submitted (11-OCT-1995) Jun Ueki, Japan Tobacco Inc., Plant Breeding and Genetics Research Lab; 700 Higashibara, Iwata, Shizuoka 438-0802, Japan (E-mail:Jun.Ueki@bgrl.jti.co.jp, Tel:81-538-33-7111, Fax:81-538-32-8700)  
 FEATURES Location/Qualifiers  
 source 1..2990  
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 /translation="MAQMLHGTLHATIFPAASISNPBASGSKPRIRKFGIEITVGVGKATKXVSTIDLEKAVGRTMTNPIINRYSKSHITCAHNASVITFKIDNPIGATNIGRAYLFPVQELNGEIDRMWDICDNNRESVSGSKLHVKLQYDVSKDRNWARGVRSKYGVGVPYTFPSQROGCKVTLVYDAHVEDNFIPIPLADGKVEPRKWCWEDIFDAISNAQHLIYITGMSVTEITLVRDSNPKPGGDTLGLLELKKASGVRLMTVMDDRTSVGLLRKDGCMVTHDEETENYFHSQVNCVLCPRNDSGSIQVDSISITMFTPHOKTIVVDHDELPHNGSQORRIVSPVGLDIDCGYDIOVHSLPRTLDSTHDDPHQNFATASIKKGGPREPMHDIHSRLRSGPIAWDLVNEQWRKQCGKDLLQLRDSDTIIIPSPWMPEREETNNVOLFPSIDGAFGFPDTEBAKGLVSGKQIIDRSIQDAYIHARRAKNTIYENQYFLGSSYAMKEGKPEPIDGLHLIPKELAKVSKLEAGERFTYVVVPMWPEGVPEBSVOALIDMQRTMWMYDITLALAKGLEANKDYLTFFCLGNREVKQAGEYQPEQPADYDSRAQARRPMIYVHTKMMIIVDEYIITISANINQRSMWDGDESEIMAGYOPYHLATROPARGHGFMAWYELHGMIDVDFQRPSELECYCKVNRILAKYMDMYSDDLQDDLPEHLISYPLGVASDGVTEVTPMEYFPDTRARV LKASDPMPEILITS"

BASE COUNT 734 a 724 c 783 g 749 t  
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 Best Local Similarity 100.0%; Pred. No. 3.5e-09;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGCGCA 614  
 Db 288 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGCGCA 326

RESULT 11  
 LOCUS AR005011 3040 bp DNA linear PAT 04-DEC-1998  
 DEFINITION Sequence 1 from patent US 5747327.  
 ACCESSION AR005011  
 VERSION AR005011.1 GI:3965890  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 3040)  
 AUTHORS Ueki,J. and Morioke,S.  
 JOURNAL TITLE Phospholipase D gene originated from plant  
 FEATURES Patent: US 5747327-A 1 05-MAY-1998;  
 Location/Qualifiers  
 source 1..3040  
 /organism="unknown"  
 BASE COUNT 784 a 724 c 783 g 749 t  
 ORIGIN  
 Query Match 6.4%; Score 39; DB 6; Length 3040;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-09;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGCGCA 614

Db 288 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGCGCA 326

RESULT 12  
 LOCUS AR037062 3040 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 2 from patent US 5801016.  
 ACCESSION AR037062  
 VERSION AR037062.1 GI:5954918  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 3040)  
 AUTHORS Morioke,S. and Ueki,J.  
 JOURNAL TITLE DNA fragment, recombinant vector containing the same  
 expressing foreign genes using the same  
 Patent: US 5801016-A 2 01-SEP-1998;  
 Location/Qualifiers  
 source 1..3040  
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 BASE COUNT 784 a 724 c 783 g 749 t  
 ORIGIN  
 Query Match 6.4%; Score 39; DB 6; Length 3040;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-09;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 288 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGCGCA 326

RESULT 13  
 LOCUS AR082616 3040 bp DNA linear PAT 31-AUG-2000  
 DEFINITION Sequence 1 from patent US 5973226.  
 ACCESSION AR082616  
 VERSION AR082616.1 GI:10009336  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 3040)  
 AUTHORS Ueki,J. and Morioke,S.  
 JOURNAL TITLE Method of changing the composition of the phospholipid produced by  
 the living body and recombinant vector therefor  
 Patent: US 5973226-A 1 26-OCT-1999;  
 Location/Qualifiers  
 source 1..3040  
 /organism="unknown"  
 BASE COUNT 784 a 724 c 783 g 749 t  
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 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGCGCA 614  
 Db 288 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGCGCA 326

RESULT 14  
 LOCUS AC087149 172224 bp DNA linear HTG 09-DEC-2000  
 DEFINITION Mus musculus clone RP23-31016, WORKING DRAFT SEQUENCE, 17 unordered  
 pieces.  
 ACCESSION AC087149  
 VERSION AC087149.1 GI:11610875  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Mus musculus.



ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 172224)  
TITLE DOE Joint Genome Institute.  
JOURNAL Sequencing of Mouse  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 172224)  
TITLE DOE Joint Genome Institute.  
JOURNAL Direct Submission  
COMMENT Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov  
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Project Information  
Center Project Name: 1856110  
Center clone name: RPCI-23\_31016  
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Summary Statistics  
Consensus quality: 160964 bases at least Q40  
Consensus quality: 164326 bases at least Q30  
Consensus quality: 166482 bases at least Q20  
Estimated insert size: 200000; agarose-fp estimation  
Estimated insert size: 170624; sum-of-ctgigs estimation  
Quality coverage: 10.97 in Q20 bases; agarose-fp estimation  
Quality coverage: 12.86 in Q20 bases; sum-of-ctgigs estimation  
NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.  
1 1216: contig of 1216 bp in length  
1217 1316: gap of unknown length  
1317 2574: contig of 1258 bp in length  
2575 2674: gap of unknown length  
2675 3683: contig of 1009 bp in length  
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3784 6495: contig of 2712 bp in length  
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6596 9535: contig of 2940 bp in length  
9536 9635: gap of unknown length  
9636 11503: contig of 1868 bp in length  
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11604 15360: contig of 3757 bp in length  
15361 15460: gap of unknown length  
15461 26040: contig of 10580 bp in length  
26041 26140: gap of unknown length  
26141 34081: contig of 7941 bp in length  
34082 34181: gap of unknown length  
34182 41297: contig of 7116 bp in length  
41298 41397: gap of unknown length  
41398 52430: contig of 11033 bp in length  
52431 52530: gap of unknown length  
52531 62495: contig of 9965 bp in length  
62496 62595: gap of unknown length  
62596 76211: contig of 13616 bp in length  
76212 76311: gap of unknown length  
76312 94978: contig of 18667 bp in length  
94979 95078: gap of unknown length  
95079 112137: contig of 17059 bp in length  
112138 112237: gap of unknown length  
112338 131641: contig of 19404 bp in length  
131642 131741: gap of unknown length  
131742 172224: contig of 40483 bp in length.  
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1. 172224  
/organism="Mus musculus"

/db\_xref="taxon:10090"  
/clone="RP23-31016"  
/clone\_1b="RPCI mouse BAC library 23"  
BASE COUNT 49441 a 35670 c 35364 g 50148 t 1601 others  
ORIGIN  
Query Match 4.1%; Score 25; DB 2; Length 172224;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 68 TTGGCTTGGCTTTCTTTCTTTGT 92  
Db 11486 TTGGCTTGGCTTTCTTTCTTTGT 11462  
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RESULT 15  
AC094071  
LOCUS  
DEFINITION Rattus norvegicus clone CH230-10893, \*\*\* SEQUENCING IN PROGRESS  
AC094071  
AC094071.4 GI:21729029  
VERSION  
AC094071  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE  
Norway rat.  
ORGANISM Rattus norvegicus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus  
1 (bases 1 to 190039)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Alt-osman,F.R., Allen,C., Alsbrooks,S.L., Amaraltinge,H.C., Are,J.R., Ayale,M., Banks,T., Barbieri,J., Benton,J., Bimaga,K., Blankenburg,K., Bonini,D., Bouck,J., Bowe,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinu,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Eamhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huiyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovari,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louleed,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Mageshwaril,M., Mapua,P., Martin,R., Martindale,A., Martinez,B., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nockenkwo,S., Ogunh,M., Okunom,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rivers,M., Rojas,A., Rojupokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,G., Shooshari,N., Sisson,I., Sodergren,E., Sonike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansley,J., Taylor,C., Taylor,T., Teiford,B., Thomas,N., Thomas,S., Usmani,K., Vasequez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wleczky,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.  
Direct Submission  
Unpublished  
JOURNAL 2 (bases 1 to 190039)  
REFERENCE  
AUTHORS Worley,K.C.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Direct Submission  
Submitted (14-SEP-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
3 (bases 1 to 190039)  
Worley, K.C.  
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 11, 2002 this sequence version replaced gi:17972929.

----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information -----  
Center project name: GGU0  
Center clone name: CH230-108K9  
----- Summary Statistics -----  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 124193 bases at least Q40  
Consensus quality: 137621 bases at least Q30  
Consensus quality: 147568 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 68 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

1 1017: contig of 1017 bp in length  
1018 1117: gap of unknown length  
1118 2734: contig of 1617 bp in length  
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9242 10460: contig of 1219 bp in length  
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11842 11941: gap of unknown length  
11943 13139: contig of 1198 bp in length  
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13240 14617: contig of 1378 bp in length  
14618 14717: gap of unknown length  
14719 17252: contig of 2535 bp in length  
17253 17353: gap of unknown length  
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26610 27444: contig of 1135 bp in length  
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37070 39124: contig of 2056 bp in length  
39125 39224: gap of unknown length  
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46620 48139: contig of 1521 bp in length  
48140 48239: gap of unknown length  
48240 49628: contig of 1389 bp in length  
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90174 90273: contig of 2235 bp in length  
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93180 93279: contig of 2906 bp in length  
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99071 99170: contig of 2601 bp in length  
99171 101426: gap of unknown length  
101427 101526: contig of 2226 bp in length  
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Query Match

4.1%; Score 25; DB 2; Length 190039;

Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 308 TGTGTGATGTGTGTGTGTGTGT 332  
|||||  
Db 7166 TGTGTGATGTGTGTGTGTGTGT 7190

Search completed: April 3, 2003, 12:28:34  
Job time : 2349 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 10:27:58 ; Search time 212 Seconds

(without alignments)  
6522.297 Million cell updates/sec

Title: US-09-856-725-2

Perfect score: 614  
Sequence: 1 ccgcgcgcagcggaagcgcc.....ggacactcgtgggtgcgcga 614

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_101002:\*

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- 23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	614	100.0	614	22	AA82186
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3	614	100.0	2799	17	AA142854
4	540	87.9	540	22	AA82185
5	39	6.4	3040	16	AA086783
6	39	6.4	3040	17	AA142853
7	39	6.4	3040	18	AA85509
8	23	3.7	2708	16	AA086784
9	21	3.4	2970	23	AB119474

C	10	21	3.4	7862	23	AB130136	Drosophila melanog
C	11	20	3.3	999	21	AAA70234	Plasmodium falcipa
C	12	20	3.3	2115	22	AA161359	Human polynucleoti
C	13	20	3.3	2178	20	AA177111	Restriction fragme
C	14	20	3.3	2762	22	AAK94314	Human full-length
C	15	20	3.3	2970	20	AA177114	DNA sequence of GC
C	16	20	3.3	2962	22	AA099553	Human drug metabol
C	17	20	3.3	7503	21	AAA70206	Plasmodium falcipa
C	18	20	3.3	10048	24	AA067015	Human angiotensin
C	19	19	3.1	357	20	AA066421	EST clone AR440.
C	20	19	3.1	651	24	AB016108	Oligonucleotide fo
C	21	19	3.1	651	24	AB016109	Oligonucleotide fo
C	22	19	3.1	794	19	AA141443	Nucleotide sequenc
C	23	19	3.1	794	22	AA07674	Human cDNA clone A
C	24	19	3.1	840	22	AA07674	Human cDNA clone (
C	25	19	3.1	912	22	AA07674	H. pylori HPS048 e
C	26	19	3.1	921	22	AA07674	H. pylori HPC094 e
C	27	19	3.1	1305	24	ABK35529	cDNA sequence #20
C	28	19	3.1	1459	20	AA07674	Nucleotide sequenc
C	29	19	3.1	1459	20	AA07674	Human cDNA sequenc
C	30	19	3.1	2554	24	AA07674	Polynucleotide enc
C	31	19	3.1	3069	20	AA07674	Nucleotide sequenc
C	32	19	3.1	6179	22	AA07674	Tumour suppressor
C	33	19	3.1	6179	24	ABK31251	Signal transductio
C	34	19	3.1	6668	24	ABK31251	Human immune syste
C	35	19	3.1	11726	24	ABK31251	Human immune syste
C	36	19	3.1	12269	22	AA07674	Tumour suppressor
C	37	19	3.1	12269	24	ABK31251	Human immune syste
C	38	19	3.1	17419	22	AA07674	Chemically pretrea
C	39	19	3.1	17419	24	ABK31251	Human immune syste
C	40	19	3.1	17419	24	ABK31251	DNA transcription
C	41	19	3.1	17694	23	ABK31251	Drosophila melanog
C	42	19	3.1	240825	22	AA07674	Human PG-3 gene.
C	43	19	3.1	249487	24	AA07674	Mouse genomic regi
C	44	18	2.9	48	16	AA07674	Human gene signatu
C	45	18	2.9	231	23	ABK31251	Human prostatic exp
C	46	18	2.9	298	22	AA07674	Human polynucleoti
C	47	18	2.9	301	23	ABK31251	Human prostatic exp
C	48	18	2.9	386	22	ABK31251	Human nervous syst
C	49	18	2.9	400	22	ABK31251	Human nervous syst
C	50	18	2.9	400	22	ABK31251	Human nervous syst
C	51	18	2.9	400	22	ABK31251	Human nervous syst
C	52	18	2.9	417	21	AA07674	Human secreted pro
C	53	18	2.9	432	24	AA07674	Streptococcus poly
C	54	18	2.9	474	24	ABK31251	Streptococcus poly
C	55	18	2.9	474	24	ABK31251	Streptococcus poly
C	56	18	2.9	490	24	ABK31251	Human cancer relat
C	57	18	2.9	518	24	ABK31251	Oligonucleotide fo
C	58	18	2.9	518	24	ABK31251	Oligonucleotide fo
C	59	18	2.9	536	21	AA07674	Cat flea hindgut a
C	60	18	2.9	548	22	AA07674	Human cDNA clone (
C	61	18	2.9	577	24	ABK31251	Oligonucleotide fo
C	62	18	2.9	577	24	ABK31251	Oligonucleotide fo
C	63	18	2.9	621	23	ABK31251	Drosophila melanog
C	64	18	2.9	621	23	ABK31251	Arabidopsis thalia
C	65	18	2.9	681	21	AA07674	Arabidopsis thalia
C	66	18	2.9	707	24	ABK31251	Ligieria monocyot
C	67	18	2.9	761	21	AA07674	Arabidopsis thalia
C	68	18	2.9	855	20	AA07674	Human gene express
C	69	18	2.9	868	22	AA07674	Human foetal cDNA
C	70	18	2.9	932	23	ABK31251	Human prostatic exp
C	71	18	2.9	932	23	ABK31251	Human prostatic exp
C	72	18	2.9	1001	21	AA07674	Archidonic acid m
C	73	18	2.9	1096	22	ABK31251	Human membrane bou
C	74	18	2.9	1500	24	ABK31251	Bacillus lichenifo
C	75	18	2.9	1861	21	AA07674	A. thaliana gene i
C	76	18	2.9	1921	22	AA07674	Growth hormone fam
C	77	18	2.9	2019	24	ABK31251	Ligieria monocyot
C	78	18	2.9	2021	22	AA07674	Human genomic DNA
C	79	18	2.9	2077	22	AA07674	Human cDNA sequenc
C	80	18	2.9	2138	23	ABK31251	Drosophila melanog
C	81	18	2.9	2391	23	AA07674	DNA encoding novel
C	82	18	2.9	2615	23	ABK31251	Drosophila melanog

C 83	18	2.9	2679	24	ABO70862	Listeria monocytog
C 84	18	2.9	2810	8	AAW70218	Leu2 gene of Y. lip
C 85	18	2.9	2810	8	AAO83184	Yarrowia lipolytic
C 86	18	2.9	2825	23	ABL20098	Drosophila melanog
C 87	18	2.9	3561	23	ABL13848	Drosophila melanog
C 88	18	2.9	4895	23	ABL11702	Drosophila melanog
C 89	18	2.9	5001	24	ABL54374	Chemically treated
C 90	18	2.9	5001	24	ABK33951	Human DNA for stag
C 91	18	2.9	5208	24	ABL32922	Human immune syste
C 92	18	2.9	5208	24	ABL32874	Human immune syste
C 93	18	2.9	5296	24	ABL32874	Human immune syste
C 94	18	2.9	5529	24	ABL32874	Human immune syste
C 95	18	2.9	5529	24	ABL32874	Human immune syste
C 96	18	2.9	5771	24	ABN80072	DNA encoding plas
C 97	18	2.9	5856	24	ABK39988	Human chemically m
C 98	18	2.9	5928	22	AA546765	Human chemically p
C 99	18	2.9	5928	22	AA546765	Human immune syste
C 100	18	2.9	6041	24	ABL34238	Human immune syste
C 101	18	2.9	6072	24	ABD83377	Human chemically t
C 102	18	2.9	6091	24	ABD83377	Human immune syste
C 103	18	2.9	6091	24	ABD83377	Human immune syste
C 104	18	2.9	6113	24	ABO67138	Human angio genesis
C 105	18	2.9	6113	24	ABK32802	Human immune syste
C 106	18	2.9	6154	24	AA78867	Human immune syste
C 107	18	2.9	6154	24	AA78867	Human immune syste
C 108	18	2.9	6154	24	AA78867	Human immune syste
C 109	18	2.9	6289	24	ABK31200	Chemically treated
C 110	18	2.9	6310	24	ABK33029	Human gene regulat
C 111	18	2.9	6310	24	ABU70321	Human immune syste
C 112	18	2.9	6310	24	ABK31268	Chemically treated
C 113	18	2.9	6381	24	ABK31364	Signal transductio
C 114	18	2.9	6381	24	ABU70243	Chemically treated
C 115	18	2.9	6381	24	ABK32966	Human immune syste
C 116	18	2.9	6541	24	ABK34518	Human immune syste
C 117	18	2.9	6541	24	ABN80029	Human chemically m
C 118	18	2.9	6631	24	ABK28340	DNA transcripction
C 119	18	2.9	6669	24	ABU92197	Chemically treated
C 120	18	2.9	6669	24	ABU92197	Human polynucleoti
C 121	18	2.9	6669	24	ABU92197	Human immune syste
C 122	18	2.9	6669	24	ABU92197	Chemically treated
C 123	18	2.9	6740	24	ABL32193	Human immune syste
C 124	18	2.9	6740	24	ABL32193	Human immune syste
C 125	18	2.9	6971	24	ABN80061	Human immune syste
C 126	18	2.9	7165	24	ABL70222	Human digestive sy
C 127	18	2.9	7165	24	ABL70222	Chemically treated
C 128	18	2.9	7165	24	ABL70222	Human immune syste
C 129	18	2.9	7384	24	ABK31267	Signal transductio
C 130	18	2.9	7781	24	ABL32746	Human immune syste
C 131	18	2.9	7849	24	ABL32746	Human immune syste
C 132	18	2.9	7942	23	ABL22279	Human immune syste
C 133	18	2.9	8148	24	ABO71072	Chemically treated
C 134	18	2.9	8148	24	ABO71072	Drosophila melanog
C 135	18	2.9	8923	22	ABK33687	Listeria monocytog
C 136	18	2.9	9007	22	AAK87591	Human immune syste
C 137	18	2.9	9243	24	ABN60195	Human immune/haema
C 138	18	2.9	9243	24	ABN60195	Tumour suppressor
C 139	18	2.9	9568	22	ABK28254	Human chemically m
C 140	18	2.9	10072	23	ABAI9058	DNA transcripction
C 141	18	2.9	10770	22	ABU11386	Human nervous syst
C 142	18	2.9	10770	22	AA532561	Drosophila melanog
C 143	18	2.9	11169	22	AAK79181	Human immune/haema
C 144	18	2.9	11169	22	AAK79181	Human immune/haema
C 145	18	2.9	11337	22	AA528662	Human angio genesis
C 146	18	2.9	11337	22	AA528662	Genomic sequence #
C 147	18	2.9	11766	22	ABK28643	Tumour suppressor
C 148	18	2.9	11766	22	ABK28643	Human nervous syst
C 149	18	2.9	12069	24	ABK34063	Human immune syste
C 150	18	2.9	12275	23	ABK39931	Human chemically p
C 151	18	2.9	12613	22	ABU16504	Drosophila melanog
C 152	18	2.9	13125	22	AA532560	Human immune/haema
C 153	18	2.9	13125	22	AAK79178	Human immune/haema
C 154	18	2.9	13125	24	ABU70284	Chemically treated
C 155	18	2.9	13125	24	ABU70284	Human immune syste
C 156	18	2.9	13125	24	ABU70284	Human immune syste
C 157	18	2.9	13125	24	ABU70284	Human immune syste
C 158	18	2.9	13125	24	ABU70284	Human immune syste
C 159	18	2.9	13125	24	ABU70284	Human immune syste
C 160	18	2.9	13125	24	ABU70284	Human immune syste
C 161	18	2.9	13125	24	ABU70284	Human immune syste
C 162	18	2.9	13125	24	ABU70284	Human immune syste
C 163	18	2.9	13125	24	ABU70284	Human immune syste
C 164	18	2.9	13125	24	ABU70284	Human immune syste
C 165	18	2.9	13125	24	ABU70284	Human immune syste
C 166	18	2.9	13125	24	ABU70284	Human immune syste
C 167	18	2.9	13125	24	ABU70284	Human immune syste
C 168	18	2.9	13125	24	ABU70284	Human immune syste
C 169	18	2.9	13125	24	ABU70284	Human immune syste
C 170	18	2.9	13125	24	ABU70284	Human immune syste
C 171	18	2.9	13125	24	ABU70284	Human immune syste
C 172	18	2.9	13125	24	ABU70284	Human immune syste
C 173	18	2.9	13125	24	ABU70284	Human immune syste
C 174	18	2.9	13125	24	ABU70284	Human immune syste
C 175	18	2.9	13125	24	ABU70284	Human immune syste
C 176	18	2.9	13125	24	ABU70284	Human immune syste
C 177	18	2.9	13125	24	ABU70284	Human immune syste
C 178	18	2.9	13125	24	ABU70284	Human immune syste
C 179	18	2.9	13125	24	ABU70284	Human immune syste
C 180	18	2.9	13125	24	ABU70284	Human immune syste
C 181	18	2.9	13125	24	ABU70284	Human immune syste
C 182	18	2.9	13125	24	ABU70284	Human immune syste
C 183	18	2.9	13125	24	ABU70284	Human immune syste
C 184	18	2.9	13125	24	ABU70284	Human immune syste
C 185	18	2.9	13125	24	ABU70284	Human immune syste
C 186	18	2.9	13125	24	ABU70284	Human immune syste
C 187	18	2.9	13125	24	ABU70284	Human immune syste
C 188	18	2.9	13125	24	ABU70284	Human immune syste
C 189	18	2.9	13125	24	ABU70284	Human immune syste
C 190	18	2.9	13125	24	ABU70284	Human immune syste
C 191	18	2.9	13125	24	ABU70284	Human immune syste
C 192	18	2.9	13125	24	ABU70284	Human immune syste
C 193	18	2.9	13125	24	ABU70284	Human immune syste
C 194	18	2.9	13125	24	ABU70284	Human immune syste
C 195	18	2.9	13125	24	ABU70284	Human immune syste
C 196	18	2.9	13125	24	ABU70284	Human immune syste
C 197	18	2.9	13125	24	ABU70284	Human immune syste
C 198	18	2.9	13125	24	ABU70284	Human immune syste
C 199	18	2.9	13125	24	ABU70284	Human immune syste
C 200	18	2.9	13125	24	ABU70284	Human immune syste
C 201	18	2.9	13125	24	ABU70284	Human immune syste
C 202	18	2.9	13125	24	ABU70284	Human immune syste
C 203	18	2.9	13125	24	ABU70284	Human immune syste
C 204	18	2.9	13125	24	ABU70284	Human immune syste
C 205	18	2.9	13125	24	ABU70284	Human immune syste
C 206	18	2.9	13125	24	ABU70284	Human immune syste
C 207	18	2.9	13125	24	ABU70284	Human immune syste
C 208	18	2.9	13125	24	ABU70284	Human immune syste
C 209	18	2.9	13125	24	ABU70284	Human immune syste
C 210	18	2.9	13125	24	ABU70284	Human immune syste
C 211	18	2.9	13125	24	ABU70284	Human immune syste
C 212	18	2.9	13125	24	ABU70284	Human immune syste
C 213	18	2.9	13125	24	ABU70284	Human immune syste
C 214	18	2.9	13125	24	ABU70284	Human immune syste
C 215	18	2.9	13125	24	ABU70284	Human immune syste
C 216	18	2.9	13125	24	ABU70284	Human immune syste
C 217	18	2.9	13125	24	ABU70284	Human immune syste
C 218	18	2.9	13125	24	ABU70284	Human immune syste
C 219	18	2.9	13125	24	ABU70284	Human immune syste
C 220	18	2.9	13125	24	ABU70284	Human immune syste
C 221	18	2.9	13125	24	ABU70284	Human immune syste
C 222	18	2.9	13125	24	ABU70284	Human immune syste
C 223	18	2.9	13125	24	ABU70284	Human immune syste
C 224	18	2.9	13125	24	ABU70284	Human immune syste
C 225	18	2.9	13125	24	ABU70284	Human immune syste
C 226	18	2.9	13125	24	ABU70284	Human immune syste
C 227	18	2.9	13125	24	ABU70284	Human immune syste
C 228	18	2.9	13125	24	ABU70284	Human immune syste

C 229	18	2.9	161425	22	AAH02340	Human AKAP10 gene
C 230	18	2.9	162025	22	AAH02339	Human AKAP10 gene
C 231	18	2.9	162025	24	AAH028758	Human AKAP allele
C 232	18	2.9	162025	24	AAH028759	Human AKAP allele
C 233	18	2.9	174424	24	ABL68122	Ovary cancer relat
C 234	18	2.9	2155561	24	ABN71527	Streptococcus poly
C 235	17	2.8	193	22	AAK55130	Human immune/haema
C 236	17	2.8	194	22	AAK65167	Human immune/haema
C 237	17	2.8	202	21	AAK31488	Human secreted pro
C 238	17	2.8	204	22	AAK32917	Human genomic DNA
C 239	17	2.8	204	22	AAK05568	Human reproductive
C 240	17	2.8	204	22	AAK05569	Human reproductive
C 241	17	2.8	250	21	AAK27953	Human secreted pro
C 242	17	2.8	251	18	AAK65079	Canine genomic mic
C 243	17	2.8	261	21	AAK17816	Microsatellite rep
C 244	17	2.8	275	24	ABL66392	Lung cancer relat
C 245	17	2.8	275	24	ABL66392	Lung cancer relat
C 246	17	2.8	294	16	AAK75203	Human gene signatu
C 247	17	2.8	357	23	AAK75203	Human gene signatu
C 248	17	2.8	358	20	AAK90405	Human prostate exp
C 249	17	2.8	372	22	AAK189036	Human prostate exp
C 250	17	2.8	374	23	AAK189036	Human prostate exp
C 251	17	2.8	376	23	AAK189036	Human prostate exp
C 252	17	2.8	384	22	AAK78593	Human prostate exp
C 253	17	2.8	384	22	AAK78593	Human prostate exp
C 254	17	2.8	387	22	AAK60815	Human immune/haema
C 255	17	2.8	387	22	AAK60815	Human immune/haema
C 256	17	2.8	394	21	AAK10759	Fusarium venenatum
C 257	17	2.8	401	23	AAK08860	Human prostate exp
C 258	17	2.8	407	23	AAK18182	Human prostate exp
C 259	17	2.8	408	23	AAK01406	Human prostate exp
C 260	17	2.8	411	23	AAK31745	Human prostate exp
C 261	17	2.8	419	23	AAK38752	Human prostate exp
C 262	17	2.8	427	24	ABN16332	Human ORFX polynuc
C 263	17	2.8	435	22	AAK75569	Human immune/haema
C 264	17	2.8	438	23	AAK78598	Human prostate exp
C 265	17	2.8	441	22	AAK129087	Colon tumour relat
C 266	17	2.8	447	23	AAK08698	Human prostate exp
C 267	17	2.8	456	24	ABL93768	Arabidopsis thalia
C 268	17	2.8	465	23	AAK79790	Human prostate exp
C 269	17	2.8	467	21	AAK80245	Human colon cancer
C 270	17	2.8	468	22	AAK54063	Murine transport a
C 271	17	2.8	471	24	ABU93407	Arabidopsis thalia
C 272	17	2.8	482	23	ABV36061	Human prostate exp
C 273	17	2.8	482	23	ABV45120	Human prostate exp
C 274	17	2.8	492	24	ABL84183	Human ovarian canc
C 275	17	2.8	498	21	AAK16346	Human prostate can
C 276	17	2.8	499	22	AAK79371	Human prostate can
C 277	17	2.8	499	22	AAK79372	Human immune/haema
C 278	17	2.8	506	23	ABV07842	Human prostate exp
C 279	17	2.8	507	24	ABO40620	Oligonucleotide fo
C 280	17	2.8	507	24	ABO40621	Oligonucleotide fo
C 281	17	2.8	507	24	ABO40621	Oligonucleotide fo
C 282	17	2.8	511	22	AAK77646	Human ovarian canc
C 283	17	2.8	531	23	ABV39274	Human immune/haema
C 284	17	2.8	554	23	ABV37767	Human prostate exp
C 285	17	2.8	558	23	ABV40713	Human prostate exp
C 286	17	2.8	560	24	ABL36936	Human prostate exp
C 287	17	2.8	582	22	ABK64349	Human foetal liver
C 288	17	2.8	586	20	AAK20480	Human secreted pro
C 289	17	2.8	591	24	ABN63359	Human cancer relat
C 290	17	2.8	597	23	ABV54977	Human prostate exp
C 291	17	2.8	602	24	ABO66375	Arabidopsis thalia
C 292	17	2.8	618	22	AAK31468	Human DNA for a no
C 293	17	2.8	618	22	ABO66792	Human polynucleoti
C 294	17	2.8	629	24	ABO36148	Oligonucleotide fo
C 295	17	2.8	629	24	ABO36149	Oligonucleotide fo
C 296	17	2.8	660	24	ABK63119	Rat sequence diffe
C 297	17	2.8	661	22	AAK05652	Human secreted pro
C 298	17	2.8	698	24	ABO26990	Oligonucleotide fo
C 299	17	2.8	698	24	ABO26991	Oligonucleotide fo
C 300	17	2.8	700	22	AAK93255	Human inflammatory
C 301	17	2.8	706	21	AAK36936	Arabidopsis thalia
C 302	17	2.8	738	22	AAH08255	Human CDNA clone (
C 303	17	2.8	745	24	ABQ28594	Oligonucleotide fo
C 304	17	2.8	745	24	ABQ28595	Oligonucleotide fo
C 305	17	2.8	752	20	AAK22322	Human secreted pro
C 306	17	2.8	764	24	ABQ22030	Oligonucleotide fo
C 307	17	2.8	764	24	ABQ22031	Oligonucleotide fo
C 308	17	2.8	787	22	AAK197435	Human neuroblastom
C 309	17	2.8	795	24	ABQ33774	Oligonucleotide fo
C 310	17	2.8	820	20	AAK16411	Oligonucleotide fo
C 311	17	2.8	833	24	ABQ89438	Human gene express
C 312	17	2.8	903	20	AAK37526	Human prostate exp
C 313	17	2.8	930	22	AAK99416	Human secreted pro
C 314	17	2.8	1014	21	AAK05050	Met A oligonucleot
C 315	17	2.8	1053	24	ABQ23726	Arabidopsis thalia
C 316	17	2.8	1053	24	ABQ23727	Oligonucleotide fo
C 317	17	2.8	1093	22	AAK94489	Oligonucleotide fo
C 318	17	2.8	1192	24	ABQ68954	Human foetal CDNA,
C 319	17	2.8	1201	23	ABV21155	Listeria monocytog
C 320	17	2.8	1201	23	ABV21155	Human prostate exp
C 321	17	2.8	1201	23	ABV22339	Human prostate exp
C 322	17	2.8	1201	23	ABV28163	Human prostate exp
C 323	17	2.8	1230	21	AAK40784	Arabidopsis thalia
C 324	17	2.8	1257	24	ABQ39832	Oligonucleotide fo
C 325	17	2.8	1257	24	ABQ39833	Oligonucleotide fo
C 326	17	2.8	1297	22	AAK65031	Membrane-bound pro
C 327	17	2.8	1297	22	AAK65031	Human DNA encoding
C 328	17	2.8	1297	22	AAK65031	Human DNA encoding
C 329	17	2.8	1297	22	AAK65031	Human PRO791 (UNO4
C 330	17	2.8	1297	24	ABK56531	Human angiotensin
C 331	17	2.8	1297	24	ABK56531	Human PRO791 CDNA
C 332	17	2.8	1302	21	AAK47214	Arabidopsis thalia
C 333	17	2.8	1302	21	AAK47214	Arabidopsis thalia
C 334	17	2.8	1307	23	AAK55779	Human immune syste
C 335	17	2.8	1327	23	ABV25031	Human prostate exp
C 336	17	2.8	1350	21	AAK99029	Human TGC39 nucle
C 337	17	2.8	1362	21	AAK99031	Human TGC38 nucle
C 338	17	2.8	1377	21	AAK55190	Human secreted pro
C 339	17	2.8	1377	22	AAK35027	Human colon cancer
C 340	17	2.8	1377	24	ABK90714	Human polynucleoti
C 341	17	2.8	1382	23	ABL13839	Drosophila melanog
C 342	17	2.8	1386	24	ABK66714	Streptococcus poly
C 343	17	2.8	1467	21	AAK38588	Arabidopsis thalia
C 344	17	2.8	1473	21	AAK50315	Arabidopsis thalia
C 345	17	2.8	1534	22	AAK59549	Human polynucleoti
C 346	17	2.8	1535	21	AAK293355	Sequence encoding
C 347	17	2.8	1544	19	AAK296343	S. pneumoniae deriv
C 348	17	2.8	1650	23	AAK73204	DNA encoding novel
C 349	17	2.8	1706	20	AAK37335	Coffee storage pro
C 350	17	2.8	1707	21	AAK252500	Human secreted pro
C 351	17	2.8	1711	21	AAK47230	Arabidopsis thalia
C 352	17	2.8	1732	22	AAK91868	Human secreted pro
C 353	17	2.8	1834	24	ABK95801	Human ribosomal S1
C 354	17	2.8	1841	22	AAK16135	Human polynucleoti
C 355	17	2.8	1913	24	ABK70695	Listeria monocytog
C 356	17	2.8	1948	22	AAK75375	P. hybida pollen-
C 357	17	2.8	1948	22	AAK45741	Pectinase zinc finger
C 358	17	2.8	1951	22	AAK05602	Human secreted pro
C 359	17	2.8	1952	23	ABK24388	Human prostate exp
C 360	17	2.8	1952	23	ABK25185	Human prostate exp
C 361	17	2.8	2044	21	AAK42156	Arabidopsis thalia
C 362	17	2.8	2114	24	ABK40080	Human chemically p
C 363	17	2.8	2210	22	AAK15867	Human CDNA sequenc
C 364	17	2.8	2317	20	AAK97918	Human secreted pro
C 365	17	2.8	2437	24	ABL34351	Human immune syste
C 366	17	2.8	2490	22	AAK15227	Human CDNA sequenc
C 367	17	2.8	2597	23	ABL28050	Drosophila melanog
C 368	17	2.8	2650	22	AAK15780	Human CDNA sequenc
C 369	17	2.8	2702	23	ABL27042	Drosophila melanog
C 370	17	2.8	2766	19	AAK65261	DNA encoding a s.
C 371	17	2.8	2871	24	AAK22001	Human transporters
C 372	17	2.8	2877	24	AAK35393	Locus japonicus ja
C 373	17	2.8	2918	23	ABL26904	Drosophila melanog
C 374	17	2.8	2959	23	ABL15368	Drosophila melanog





521	17	2.8	6712	24	ABLJ32690	Human immune syste
522	17	2.8	6740	24	ABLJ3147	Human immune syste
523	17	2.8	6767	22	ASG46608	Tumour suppressor
524	17	2.8	6845	22	ABLJ5759	Human myoclokele
525	17	2.8	6866	24	ABL49319	Human polynucleoti
526	17	2.8	6866	24	ABLJ32666	Human immune syste
527	17	2.8	6912	24	ABK28372	DNA transcription
528	17	2.8	6954	24	ABLJ3391	Human immune syste
529	17	2.8	6988	24	ABLJ4440	Human immune syste
530	17	2.8	7069	22	ASG46654	Tumour suppressor
531	17	2.8	7069	24	ABO65984	Human anglogenesis
532	17	2.8	7069	24	ABL70292	Chemically treated
533	17	2.8	7069	24	ABLJ3353	Human immune syste
534	17	2.8	7069	24	ASG61220	Human gene regulat
535	17	2.8	7069	24	ABKJ1319	Signal transductio
536	17	2.8	7108	24	ABKJ9996	Human chemically p
537	17	2.8	7143	24	ABLJ32982	Human immune syste
538	17	2.8	7272	22	ASG46357	Tumour suppressor
539	17	2.8	7317	22	ASG45342	Chemically pretrea
540	17	2.8	7317	24	ABK28173	DNA transcription
541	17	2.8	7317	24	ABL19648	Drosophila melanog
542	17	2.8	7340	23	ABL14828	Drosophila melanog
543	17	2.8	7341	24	ASG61394	Human gene regulat
544	17	2.8	7348	22	ASG46336	Tumour suppressor
545	17	2.8	7359	24	ABLJ3862	Human immune syste
546	17	2.8	7498	24	ABLJ32556	Human immune syste
547	17	2.8	7498	24	ABLJ2257	Human immune syste
548	17	2.8	7534	24	ABN80154	Human chemically m
549	17	2.8	7534	24	ABN80155	Human chemically m
550	17	2.8	7644	24	ABLJ32530	Human immune syste
551	17	2.8	7674	23	ABL19650	Drosophila melanog
552	17	2.8	7843	24	ABL70476	Chemically treated
553	17	2.8	7843	24	ASG61439	Human gene regulat
554	17	2.8	7843	24	ABKJ1505	Signal transductio
555	17	2.8	7880	24	ABL70239	Chemically treated
556	17	2.8	7890	24	ASG61184	Human gene regulat
557	17	2.8	7982	23	ABL02334	Drosophila melanog
558	17	2.8	8056	22	ABK79815	Human immune/haema
559	17	2.8	8131	24	ABLJ2897	Human immune syste
560	17	2.8	8131	24	ASG63327	Chemically pretrea
561	17	2.8	8254	24	ABLJ2864	Human immune syste
562	17	2.8	8254	24	ABLJ2865	Human immune syste
563	17	2.8	8453	24	ABN80025	Human chemically m
564	17	2.8	8478	16	AAQ81792	B. subtilis biotin
565	17	2.8	8543	22	ASG45305	Chemically pretrea
566	17	2.8	8543	24	ABK28144	DNA transcription
567	17	2.8	8588	22	ASG45470	Chemically pretrea
568	17	2.8	8588	24	ABK28326	DNA transcription
569	17	2.8	8789	16	AAQ86851	Human mtocsin gene
570	17	2.8	8789	19	AAV09076	Mitocsin nucleic ac
571	17	2.8	8865	22	AAK87029	Human immune/haema
572	17	2.8	8897	24	ABL70228	Chemically treated
573	17	2.8	8943	24	ABKJ9967	Human chemically p
574	17	2.8	9176	23	ABLJ3200	Drosophila melanog
575	17	2.8	9180	24	ABLJ3964	Human immune syste
576	17	2.8	9238	24	ABK28365	DNA transcription
577	17	2.8	9370	22	AL07075	Human reproductive
578	17	2.8	9375	22	ABL37084	Human musculoskele
579	17	2.8	9375	22	AAK84379	Human immune/haema
580	17	2.8	9384	22	ABA14819	Human immune/haema
581	17	2.8	9384	22	ASG28401	Human nervous syste
582	17	2.8	9539	23	ABL15474	Genomic sequence #
583	17	2.8	9731	22	ABK72933	Drosophila melanog
584	17	2.8	9731	22	AAK85096	Human immune/haema
585	17	2.8	9733	22	AAK72935	Human immune/haema
586	17	2.8	9733	22	AAK85097	Human immune/haema
587	17	2.8	9766	24	ABK69846	Human immune/haema
588	17	2.8	9832	24	ABLJ2656	Human secreted pro
589	17	2.8	9929	22	ABA17906	Human immune syste
590	17	2.8	10034	24	ABLJ3385	Human nervous syste
591	17	2.8	10039	24	ABLJ34042	Human immune syste
592	17	2.8	10096	24	ABK70292	Human immune syste
593	17	2.8	10136	17	AAK734578	Human lung cancer
					Kinetochoe protei	
594	17	2.8	10144	24	ABL49393	Human polynucleoti
595	17	2.8	10190	24	ABK09755	Human ovarian tumo
596	17	2.8	10211	24	ABL65843	Lung cancer relat
597	17	2.8	10211	24	ABL67994	Ovary cancer relat
598	17	2.8	10281	24	ASG4946	Human DNA sequence
599	17	2.8	10326	24	ABLJ4167	Human immune syste
600	17	2.8	10433	24	ABLJ2379	Human immune syste
601	17	2.8	10433	23	ABL12312	Drosophila melanog
602	17	2.8	10622	23	ABL04256	Drosophila melanog
603	17	2.8	11186	24	AD36213	Human cytochrome P
604	17	2.8	11209	24	ABN80136	Human chemically m
605	17	2.8	11260	22	ASG45314	Chemically pretrea
606	17	2.8	11260	24	ABN80038	Human chemically m
607	17	2.8	11260	24	ABK28153	DNA transcription
608	17	2.8	11650	22	ASG46755	Tumour suppressor
609	17	2.8	11819	22	AAK81675	Human immune/haema
610	17	2.8	11836	22	ASG45294	Chemically pretrea
611	17	2.8	11836	24	ABK28239	DNA transcription
612	17	2.8	11870	22	AAV07328	Human reproductive
613	17	2.8	11870	22	AAV07329	Human reproductive
614	17	2.8	11870	22	AAK82242	Human immune/haema
615	17	2.8	11870	22	AAK82243	Human immune/haema
616	17	2.8	11870	22	AAK84792	Human immune/haema
617	17	2.8	11870	22	AAK84793	Human immune/haema
618	17	2.8	12237	24	ABLJ4358	Human immune syste
619	17	2.8	12278	22	ABA14585	Human nervous syste
620	17	2.8	12278	22	ABA14664	Human nervous syste
621	17	2.8	12356	22	ASG46510	Tumour suppressor
622	17	2.8	12396	23	ABL16560	Drosophila melanog
623	17	2.8	12669	24	ABL70490	Chemically treated
624	17	2.8	12669	24	ASG61449	Human gene regulat
625	17	2.8	12669	24	ABKJ1523	Signal transductio
626	17	2.8	12705	24	ABLJ2149	Human immune syste
627	17	2.8	12763	24	ABLJ3303	Human immune syste
628	17	2.8	13249	24	ABL70131	Chemically treated
629	17	2.8	13249	24	ABLJ2116	Human immune syste
630	17	2.8	13249	24	ABKJ1176	Signal transductio
631	17	2.8	13420	24	ABLJ2916	Human immune syste
632	17	2.8	13427	24	ABLJ33926	Human immune syste
633	17	2.8	13449	24	ABLJ3385	Human immune syste
634	17	2.8	13449	24	ABLJ3385	Human immune syste
635	17	2.8	13574	24	ABLJ3317	Human immune syste
636	17	2.8	13578	22	AAK81662	Human immune/haema
637	17	2.8	13909	23	ABL20392	Drosophila melanog
638	17	2.8	13948	22	AAK75938	Human immune/haema
639	17	2.8	13940	22	AAK75915	Human immune syste
640	17	2.8	14253	24	ABLJ3494	Human tumour suppre
641	17	2.8	15399	24	ABLJ33514	Human immune syste
642	17	2.8	15399	24	ABLJ33514	Human immune syste
643	17	2.8	15518	24	ABL70607	Chemically treated
644	17	2.8	15518	24	ABLJ4624	Human immune syste
645	17	2.8	15674	24	ABL70514	Chemically treated
646	17	2.8	15674	24	ABLJ2363	Human immune syste
647	17	2.8	15674	24	ABLJ4477	Human immune syste
648	17	2.8	15782	24	ABK28135	DNA transcription
649	17	2.8	15861	24	ABLJ2525	Human immune syste
650	17	2.8	16167	24	ABL70253	Chemically treated
651	17	2.8	16167	24	ABLJ3082	Human immune syste
652	17	2.8	16167	24	ABLJ34528	Human immune syste
653	17	2.8	16170	24	ABLJ3369	Human immune syste
654	17	2.8	16618	22	ASG34721	Human DNA for a no
655	17	2.8	16688	22	ASG46555	Tumour suppressor
656	17	2.8	16724	24	ABL70259	Chemically treated
657	17	2.8	16724	24	ABLJ3090	Human immune syste
658	17	2.8	16724	24	ABLJ3090	Human immune syste
659	17	2.8	16724	24	ABLJ34536	Human immune syste
660	17	2.8	17213	24	ABLJ3483	Human immune syste
661	17	2.8	17234	24	ASG67017	Human anglogenesis
662	17	2.8	17419	22	ASG45392	Chemically pretrea
663	17	2.8	17419	24	ABLJ33294	Human immune syste
664	17	2.8	17419	24	ABK28337	DNA transcription
665	17	2.8	17677	22	AAK70506	Human immune/haema
666	17	2.8	17721	22	AAK84095	Human immune/haema
					ABLJ33728	Human immune syste



C 813	16	2.6	329	22	AA190344	Human polynucleoti	886	16	2.6	394	24	ABN95557	Gene #2055 used to
C 814	16	2.6	330	22	AA538058	Novel human diagno	887	16	2.6	395	22	AA110568	Human breast cancer
C 815	16	2.6	330	22	AA191961	Human polynucleoti	C 888	16	2.6	396	22	AA189002	Human polynucleoti
C 816	16	2.6	332	22	AA182716	Human polynucleoti	889	16	2.6	396	24	ABN96766	Gene #3264 used to
C 817	16	2.6	332	22	AAH93305	Plasmodium falcipa	890	16	2.6	396	24	ABN77945	Human ORF2892 cDNA
C 818	16	2.6	339	16	AA226630	Human gene signatu	C 891	16	2.6	397	22	AAK76988	Human immune/haema
C 819	16	2.6	341	22	AA539934	Genomic sequence #	C 892	16	2.6	397	22	AAK76989	Human immune/haema
C 820	16	2.6	341	22	AA182886	Human polynucleoti	C 893	16	2.6	398	14	AAQ46001	NPS-331. Tegenari
C 821	16	2.6	341	22	AAK75093	Human immune/haema	C 894	16	2.6	398	16	AAQ96073	Polypeptide compon
C 822	16	2.6	341	22	AAK75094	Human immune/haema	C 895	16	2.6	398	19	AAV52920	Tegenaria agrestis
C 823	16	2.6	341	22	AAK90378	Human digestive sy	896	16	2.6	399	21	AAK23997	Human secreted pro
C 824	16	2.6	345	24	ABN18085	Human ORF polynuc	C 897	16	2.6	400	22	AA184626	Human polynucleoti
C 825	16	2.6	346	22	AA187279	Human polynucleoti	C 898	16	2.6	401	22	AAK96224	Human neutregulin g
C 826	16	2.6	348	22	AAH36014	Human colon cancer	C 899	16	2.6	401	22	AAK97117	Human neutregulin g
C 827	16	2.6	349	22	AA189583	Human polynucleoti	900	16	2.6	401	22	AA181262	Human polynucleoti
C 828	16	2.6	352	14	AAQ59500	Human brain Expres	901	16	2.6	402	14	ABM63179	Human cancer relat
C 829	16	2.6	352	21	AAA74246	Lobolilly pine SSR	C 902	16	2.6	402	14	AAQ59630	Human cancer relat
C 830	16	2.6	352	21	AAQ00663	Human secreted pro	C 903	16	2.6	402	23	ABV16611	Human prostate exp
C 831	16	2.6	352	24	ABN22701	Human ORF polynuc	C 904	16	2.6	404	23	ABV33358	Human prostate exp
C 832	16	2.6	353	20	AAV89188	Human prostate exp	C 905	16	2.6	404	23	ABV42281	Human prostate exp
C 833	16	2.6	356	23	ABV12213	Human prostate exp	906	16	2.6	405	24	ABK95405	Human retina speci
C 834	16	2.6	357	24	ABN22803	Human ORF polynuc	907	16	2.6	406	21	AAQ00695	Human secreted pro
C 835	16	2.6	359	22	AB180268	Human polynucleoti	908	16	2.6	406	22	AA180165	Human polynucleoti
C 836	16	2.6	360	23	ABV04405	Human prostate exp	909	16	2.6	407	23	ABV37726	Human prostate exp
C 837	16	2.6	360	23	ABV07801	Human prostate exp	910	16	2.6	407	24	ABL82100	Human ovarian canc
C 838	16	2.6	361	22	AA100373	Human reproductive	911	16	2.6	408	22	AA189956	Human polynucleoti
C 839	16	2.6	361	22	AA186138	Human polynucleoti	912	16	2.6	410	23	ABV13810	Human prostate exp
C 840	16	2.6	361	22	AAK74908	Human immune/haema	913	16	2.6	410	23	ABV14692	Human prostate exp
C 841	16	2.6	361	22	AAK77085	Human immune/haema	914	16	2.6	410	23	ABV32858	Human prostate exp
C 842	16	2.6	363	24	ABK38840	CDNA encoding lung	915	16	2.6	410	23	ABV41783	Human prostate exp
C 843	16	2.6	364	22	AAK59754	Human immune/haema	916	16	2.6	411	23	ABV04641	Human prostate exp
C 844	16	2.6	364	24	ABK38829	CDNA encoding lung	C 917	16	2.6	411	23	ABV16730	Human prostate exp
C 845	16	2.6	365	22	AAK81731	Human immune/haema	918	16	2.6	411	23	ABV53899	Human prostate exp
C 846	16	2.6	366	22	AAK58261	Human immune/haema	C 919	16	2.6	412	21	AAK39746	Human prostate exp
C 847	16	2.6	367	22	AAK17764	Human breast cancer	C 920	16	2.6	413	12	AAQ13400	Mouse u6 intranuci
C 848	16	2.6	367	24	ABK39105	CDNA encoding lung	C 921	16	2.6	413	22	AA181756	Human polynucleoti
C 849	16	2.6	367	24	ABK39588	CDNA encoding lung	C 922	16	2.6	413	22	AA191772	Human polynucleoti
C 850	16	2.6	368	22	AA110576	Human breast cancer	C 923	16	2.6	413	23	ABV16645	Human prostate exp
C 851	16	2.6	368	24	ABO85524	Arabidopsis thalia	C 924	16	2.6	415	23	ABV19971	Human prostate exp
C 852	16	2.6	368	24	ABK38965	CDNA encoding lung	925	16	2.6	415	24	ABN96629	Gene #3127 used to
C 853	16	2.6	368	24	ABK39006	CDNA encoding lung	C 926	16	2.6	417	23	ABV17807	Human prostate exp
C 854	16	2.6	368	24	ABK39006	CDNA encoding lung	927	16	2.6	418	22	AA100952	Human reproductive
C 855	16	2.6	368	24	ABK39054	CDNA encoding lung	C 928	16	2.6	418	22	AA181105	Human polynucleoti
C 856	16	2.6	368	24	ABK39126	CDNA encoding lung	929	16	2.6	418	23	ABL96422	Human testicular a
C 857	16	2.6	369	22	ABK39546	CDNA encoding lung	930	16	2.6	419	23	ABV13400	Human prostate exp
C 858	16	2.6	369	22	AA184074	Human polynucleoti	C 931	16	2.6	420	22	AA185653	Human polynucleoti
C 859	16	2.6	369	23	ABV11713	Human prostate exp	C 932	16	2.6	420	24	ABL84117	Human ovarian canc
C 860	16	2.6	371	23	ABV03044	Human prostate exp	C 933	16	2.6	420	24	ABV14673	Human prostate exp
C 861	16	2.6	372	22	AA180729	Human polynucleoti	C 934	16	2.6	428	22	AA191354	Human polynucleoti
C 862	16	2.6	372	22	AA183395	Human polynucleoti	935	16	2.6	430	22	AAK85081	Human immune/haema
C 863	16	2.6	373	18	AA769154	Typanosoma cruzi	C 936	16	2.6	430	23	ABV17208	Human prostate exp
C 864	16	2.6	373	20	AAK81743	DNA encoding a T	937	16	2.6	431	24	AA141876	Human li beta-hydr
C 865	16	2.6	374	22	AA186270	Human polynucleoti	C 938	16	2.6	433	22	AA180712	Human polynucleoti
C 866	16	2.6	374	24	ABN97012	Gene #3510 used to	939	16	2.6	434	21	AAV74218	Lobolilly pine SSR
C 867	16	2.6	375	22	AA183872	Human polynucleoti	940	16	2.6	437	21	AAK27501	Human secreted pro
C 868	16	2.6	377	21	AAH30923	Human colon cancer	C 941	16	2.6	437	23	ABV07827	Human prostate exp
C 869	16	2.6	377	22	AA180435	Human polynucleoti	C 942	16	2.6	437	24	ABN65306	Human cancer relat
C 870	16	2.6	378	24	ABN64902	Human cancer relat	943	16	2.6	440	22	AA536131	Human cardiovascular
C 871	16	2.6	378	24	ABH58085	Human ovarian canc	C 944	16	2.6	441	21	AAFL5735	Human prostate can
C 872	16	2.6	379	22	AAH34099	Human colon cancer	945	16	2.6	441	21	AAFL5735	Human prostate can
C 873	16	2.6	380	22	AAH17643	Human breast cancer	946	16	2.6	446	21	AAFL18098	Lung cancer associ
C 874	16	2.6	381	23	ABV48657	Human prostate exp	947	16	2.6	451	23	ABV34922	Human prostate exp
C 875	16	2.6	384	24	ABL83974	Human ovarian canc	948	16	2.6	451	23	ABV43771	Human prostate exp
C 876	16	2.6	386	22	AA101612	Human reproductive	949	16	2.6	451	24	ABN76376	Human ORF1323 cDNA
C 877	16	2.6	388	22	AA181345	Human polynucleoti	C 950	16	2.6	453	22	ABH08129	Human ovarian and
C 878	16	2.6	389	22	AA180075	Human polynucleoti	C 951	16	2.6	453	22	ABH08130	Human ovarian and
C 879	16	2.6	389	22	AA183856	Human polynucleoti	C 952	16	2.6	453	22	ABA08131	Human ovarian and
C 880	16	2.6	389	24	ABN25932	Human ORF polynuc	953	16	2.6	453	22	AA536133	Human cardiovascular
C 881	16	2.6	391	22	AA117651	Human breast cancer	C 954	16	2.6	453	22	AA106910	Human reproductive
C 882	16	2.6	391	22	AA190037	Human polynucleoti	C 955	16	2.6	453	22	AA106911	Human reproductive
C 883	16	2.6	394	14	AAQ46000	NPS-326. Tegenari	C 956	16	2.6	453	22	AA106912	Human reproductive
C 884	16	2.6	394	16	AAQ96070	Polypeptide compon	C 957	16	2.6	453	23	ABV47697	Human prostate exp
C 885	16	2.6	394	19	AAV25917	Tegenaria agrestis	958	16	2.6	454	22	AAV93665	CDNA encoding SRT

Human prostate expr  
Human ovarian can  
Human breast cell  
Human foetal liver  
Probe #2277 for ge  
Human brain expres  
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Probe #2293 for ge  
Probe #2401 used t  
Probe #2263 used t  
Human genome-deriv  
Human prostate exp  
Human prostate exp  
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Gene #823 used to  
Human reproductive  
Human cancer relat  
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Human ovarian tumo  
Human immune/haema  
Human prostate exp  
Human immune/haema  
Human collagen gen  
Human prostate exp  
Human polynucleoti  
Human foetal liver  
Probe #6001 for ge  
Human brain expres  
Human bone marrow  
Probe #5951 for ge  
Probe #6777 used t  
Human genome-deriv  
Human foetal liver  
Probe #416 for gen

## ALIGNMENTS

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RESULT 1
AAF82186
ID   AAF82186 standard; DNA; 614 BP.
AC   AAF82186;
DT   02-JUL-2001 (first entry)
DE   Structural gene expression promoting related polynucleotide SEQ ID NO:2
XX   KM Rice; structural gene expression promotion; breeding; modification;.
XX   plant; ds.
XX   OS   Oryza sativa.
XX   MO200123544-A1.
XX   PN   05-APR-2001.
XX   PD   25-SEP-2000; 2000WO-JP06560.
XX   PF   27-SEP-1999; 99JP-0271762.
XX   PR
XX   PA   (N1SB ) JAPAN TOBACCO INC.
XX   DT   Ueki J, Morioka S;

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WPI; 2001-266148/27:

Claim 6; Page 8-9; 12pp; Japanese.

The present invention describes a rice nucleic acid fragment (1) which promotes the expression of a structural gene located downstream, where (1) is superior in promoting expression of structural gene located downstream. Also described are: (1) a recombinant vector containing any of the nucleic acid fragment and at least 1 structural gene at its downstream; (2) promoting expression of a structural gene at its nucleic acid fragment to its upstream; and (3) plants or their descendants who can sustain the transformation is promoting expression of desired structural genes by the above method. (1) can be used in breeding, modifying and improving plants with foreign genes introduced. The present sequence represents a rice structural gene expression promoting related polynucleotide sequence from the present invention.

Sequence 614 BP; 146 A; 114 C; 131 G; 223 T; 0 other;

Query Match	Score 614;	DB 22;	Length 614,
100.0%;			
Local Similarity	100.0%;		

614; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 CCGGCCAGCGGAAGCGCCCCCAAGTTCATCCGCAAGTTCGACCCCTTCTCCTTAACT 60

1 CCGCGCCAGCGAAGCCGCCCACTTCATCCGCAAGGTCGGACCTTCTCTCTTATCTC 60

61 ACTCGTCTTTGCTCTTGACTCTTTTTCTTTTGATGTCCCTTTTCATTCACTCATCCTACCTCTCTCTCT

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1 21 ACCCCCCC TTTTCC CCCCAC CCGGAG AG 12

TGAGTGGCTATCGACAGAACAGTCAGATAACTGAACGATCTGCAAT 18

121 AGCCGAAATTCATCTGCTAGTCACAGTACAGTACAGTACATCACTGAACGATCTGGAAT 18

181 TCTGGATTATTAGGAAAAATTAAGACGTTAGACACAGAATTGGACATCTTCTATCAA 24

181 TCTGATTATTAGAAATAAAGAGTAGTAGACACAGAATTGGAGATCTTCTATCAA 24

241 GATTGCTATTATGCTTGCCATTCTGTTGACCCAACTACTTCTTGAATCTAGAG 30

241 GATTGCTATTATGCTTGCCATTCTTGTTGACCCAGTACTCTTGAATCTAGAC 300

301 TTTCGTGTCGATGTCGTCGTGTTGTGTCACCAAAATCTTCACTTACCTTAAATCTC

TTTGGCTGTCGTATGTGGTGATGTTTGATGCTCAACCAAAATCCTCCATAAAGCGTAAT

361 AAAATTATTTAATTATACTGACCGAGCCAACTTGGCCTG  
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[illegible]

.....TATTAACGACCACTAAATAAGAGTTCTCTGTGTGATGTGCT 420

421  
1G1G1CACCAAAATCTTGATTGATGAGCTTTTATTATTATTACTGACCTACTAC 480

421 TGIGTACCACAAAATCTTGATTGATAGAGTTTATTATTATTAACTGACCTACTAC 480

481 AAATCTATTGCTGATGCTATGCTGCTCTGATACCTGAAATGCATGCTTCTTCTT 540

481 AAATCTATTGCTGATGCTATGTTGTTCTGTATCACCTGAATGCATGCTTCTTCTTT 540

541 GTTGTTCTTGATCTAACACGTCAGCTCATGTCACACGTTTGTCGAGGGGATTCACCAACG CCG

541 GTTGTCTTGATCTACACGCTGAGCTATCTCAACACTTCTCTCCACCCCAATTCCTCTT

501 TATGGGTCATCGGCA 514  
-----TCTGCAACCCGCACTTCAAGGACAC 800

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CC This sequence represents a fragment of the coding sequence of the rice  
 CC phospholipase D gene (PLD). The promoter for the PLD gene was isolated  
 CC using the primers shown in AAT42857 and AAT42588. The promoters (see  
 CC AAT42851 and AAT42852) are efficient promoters for greatly increasing the  
 CC expression of foreign genes in transformant rice and other plants.  
 XX

Sequence 2799 BP; 692 A; 709 C; 609 G; 789 T; 0 other;

Query Match 100.0%; Score 614; DB 17; Length 2799;  
 Best Local Similarity 100.0%; Pred. No. 3, 5e-286;

Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CCGGCGCCGCGGAGCGCCCAAGTTCATCCGAGGTTGGACCCCTTCTCTTATCT 60
DB 1947 CCGGCGCCGCGGAGCGCCCAAGTTCATCCGAGGTTGGACCCCTTCTCTTATCT 2006
QY 61 ACTGCTCTTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 120
DB 2007 ACTGCTCTTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2066
QY 121 AGCCCGAATTTGATCTCTAGTCAGTACAGTACATGACATGAAAGATCTGGAAT 180
DB 2067 AGCCCGAATTTGATCTCTAGTCAGTACAGTACATGACATGAAAGATCTGGAAT 2126
QY 181 TCTGATTAATAGAAATAAAGAGTACTAGCAAGAAATGGAATCTTCTATCAA 240
DB 2127 TCTGATTAATAGAAATAAAGAGTACTAGCAAGAAATGGAATCTTCTATCAA 2186
QY 241 GATTGCTATTAATGCTGGCCATTTCTTGTGACCCAGTACTCTTGTGATCTAAG 300
DB 2187 GATTGCTATTAATGCTGGCCATTTCTTGTGACCCAGTACTCTTGTGATCTAAG 2246
QY 301 TTGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 2247 TTGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2306
QY 361 AAATTTTATTTATTAACGACCTAAATAAGTAGAGTCTCTGCTGCTGCTGCT 420
DB 2307 AAATTTTATTTATTAACGACCTAAATAAGTAGAGTCTCTGCTGCTGCTGCT 2366
QY 421 TGTGTCACCAAAATCTGATTTGATAGAGTTTATTTATTTATTTATTTATTT 480
DB 2367 TGTGTCACCAAAATCTGATTTGATAGAGTTTATTTATTTATTTATTTATTT 2426
QY 481 AAATCTATTTGCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 2427 AAATCTATTTGCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2486
QY 541 GTTGTCTTGAATCTAACAAGTCACTCATGTCACAGTTTGTGAGGGGATTTGAG 600
DB 2487 GTTGTCTTGAATCTAACAAGTCACTCATGTCACAGTTTGTGAGGGGATTTGAG 600
QY 601 TGTGGGTGTGGCA 614
DB 2547 TGTGGGTGTGGCA 2560
  
```

## RESULT 4

ID AAF82185 standard; DNA; 540 BP.

XX AAF82185;

DT 02-JUL-2001 (first entry)

DE Rice structural gene expression promoting polynucleotide SEQ ID NO.1.

KW Rice; structural gene expression promotion; breeding; modification;

XX Oryza sativa.

XX OS

XX PN MO200123544-A1.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-JP06560.

XX 27-SEP-1999; 99JP-0271762.

XX (NISB) JAPAN TOBACCO INC.

XX Ueki J, Morioka S;

XX WPI; 2001-266148/27.

PT New nucleic acid fragment useful for promoting expression of structural  
 PT gene located downstream, useful in breeding, modifying and improving  
 PT plants with foreign gene introduced

PS Claim 1; Page 8; 12pp; Japanese.

CC The present sequence represents a rice nucleic acid fragment (I) which  
 CC promotes the expression of a structural gene located downstream, where  
 CC (I) is superior in promoting expression of structural gene located  
 CC downstream. Also described are: (1) a recombinant vector containing any  
 CC of the nucleic acid fragment and at least 1 structural gene at its  
 CC downstream; (2) promoting expression of a structural gene by inserting  
 CC the nucleic acid fragment to its upstream; and (3) plants or their  
 CC descendants who can sustain the transformation is promoting expression  
 CC of desired structural genes by the above method. (I) can be used in  
 CC breeding, modifying and improving plants with foreign genes introduced.  
 XX

Sequence 540 BP; 132 A; 94 C; 104 G; 210 T; 0 other;

Query Match 87.9%; Score 540; DB 22; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1, 8e-250;

Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 38 GTTCGACCCCTTCTCTTATCTAGTCTGCTCTTCTTCTTCTTCTTCTTCTTCT 97
DB 1 GTTCGACCCCTTCTCTTATCTAGTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCT 60
QY 98 TTTCTTGTGTGCTTTCATGAGCCCGAATTTGATGCTGTAGGACAGTACAG 157
DB 61 TTTCTTGTGTGCTTTCATGAGCCCGAATTTGATGCTGTAGGACAGTACAGTAC 120
QY 158 ATACACTGAAACGATCTGGAATTTCTGATTTATGAAATAAAGAGTAGTACAA 217
DB 121 ATACACTGAAACGATCTGGAATTTCTGATTTATGAAATAAAGAGTAGTACAA 180
QY 218 GAATTTGAGATATCTTCTATCAAGATGCTATTTATGCTTGGCATTCTTCTT 277
DB 181 GAATTTGAGATATCTTCTATCAAGATGCTATTTATGCTTGGCATTCTTCTT 240
QY 278 CAAGTACTCTTCTTGAATCTAGAGTTTCTGTGTGTGTGTGTGTGTGTGTGT 337
DB 241 CAAGTACTCTTCTTGAATCTAGAGTTTCTGTGTGTGTGTGTGTGTGTGTGT 300
QY 338 AAAATCTTCATTAGCTAAACGTAATTTATTTATTTATTTATTTATTTATTT 397
DB 301 AAAATCTTCATTAGCTAAACGTAATTTATTTATTTATTTATTTATTTATTT 360
QY 398 GTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 457
DB 361 GTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 458 TTATTTATTTAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 517
DB 421 TTATTTATTTAGTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 480
QY 518 TGAATGCAATGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 577
DB 481 TGAATGCAATGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 540
  
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RESULT 5
AA086783
ID AA086783 standard; cDNA to mRNA; 3040 BP.
XX
AC AA086783;
XX
DT 01-MAR-1996 (first entry)
XX
DE DNA encoding phospholipase D.
XX
KM phospholipase D; measurement; reagent; phospholipid level; ss.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT CDS 182..2620
FT /*tag= a
FT /product= phospholipase D
XX
PN WO9509234-A1.
XX
PD 06-APR-1995.
XX
PF 30-SEP-1994; 94WO-JP01627.
XX
PR 30-SEP-1993; 93JP-0267884.
XX
PA (NISR ) JAPAN TOBACCO INC.
XX
PI Morioka S, Ueki J;
XX
DR WPI; 1995-147433/19.
DR P-PSDB; AAR72797.
XX
XX
PT Cloned DNA coding plant derived phospholipase D - controls
PT expression of plant derived PLD gene
XX
XX
PS Claim 7; Page 14-19; 41pp; Japanese.
XX
CC The DNA encodes a plant derived phospholipase D (PLD). The PLD is
CC useful for measuring phospholipid levels and for producing derivs.
CC by e.g. base exchange reactions. DNA controlling the expression of
CC the plant derived PLD is also claimed and shown in AA086785.
XX
SQ Sequence 3040 BP; 784 A; 724 C; 783 G; 749 T; 0 other;

Query Match 6.4%; Score 39; DB 16; Length 3040;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 576 AGTTGTGAGGAGGATTGAGACACTGTGGGTGCGCA 614
    |||||||||||||||||||||||||||||||||||
DB 288 AGTTGTGAGGAGGATTGAGACACTGTGGGTGCGCA 326

RESULT 6
AAT42853
ID AAT42853 standard; cDNA to mRNA; 3040 BP.
XX
AC AAT42853;
XX
DT 16-JUN-1997 (first entry)
XX
DE Phospholipase D protein coding sequence.
XX
KM Phospholipase D; rice; promoter; ss.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT CDS 181..2620
FT /*tag= a
FT /product= phospholipase D

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XX
PN WO9630510-A1.
XX
PD 03-OCT-1996.
XX
PF 28-MAR-1996; 96WO-JP00812.
XX
PR 29-MAR-1995; 95JP-0096126.
XX
PA (NISR ) JAPAN TOBACCO INC.
XX
PI Morioka S, Ueki J;
XX
DR WPI; 1996-455357/45.
DR P-PSDB; AAW06134.
XX
PT Promoter DNA sequence derived from rice - used to increase
PT expression of foreign genes in transformed hosts
XX
PS Disclosure; Page 14-20; 29pp; Japanese.
XX
CC This sequence represents the coding sequence for the rice phospholipase
CC D gene (PLD). The promoter for the PLD gene was isolated using the
CC primers shown in AAT42857 and AAT42588. The promoters (see AAT42851 and
CC AAT42852) are efficient promoters for greatly increasing the expression
CC of foreign genes in transformant rice and other plants.
XX
SQ Sequence 3040 BP; 784 A; 724 C; 783 G; 749 T; 0 other;

Query Match 6.4%; Score 39; DB 17; Length 3040;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 576 AGTTGTGAGGAGGATTGAGACACTGTGGGTGCGCA 614
    |||||||||||||||||||||||||||||||||||
DB 288 AGTTGTGAGGAGGATTGAGACACTGTGGGTGCGCA 326

RESULT 7
AAT85509
ID AAT85509 standard; cDNA to mRNA; 3040 BP.
XX
AC AAT85509;
XX
DT 23-MAR-1998 (first entry)
XX
DE Phospholipase D encoding cDNA.
XX
KM Phospholipase D; phospholipid; food; medicine; rice plant;
KM monocoyledon; ds.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT CDS 182..2620
FT /*tag= a
FT /product= Phospholipase_D
XX
PN WO9731106-A1.
XX
PD 28-AUG-1997.
XX
PF 20-FEB-1997; 97WO-JP00466.
XX
PR 21-FEB-1996; 96JP-0058320.
XX
PA (NISR ) JAPAN TOBACCO INC.
XX
PI Morioka S, Ueki J;
XX
DR WPI; 1997-435159/40.
DR P-PSDB; AAW25675.
XX

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PT Changing the composition of phospholipid(s) produced by host cells -
PT produces phospholipid(s) of better usability than natural
PT phospholipid(s), applicable in food, medicine etc.
XX
PS Example 1; Page 12-17; 22pp; Japanese.
XX
CC A novel method has been developed for changing the composition of
CC phospholipids produced by host cells. The method comprises transforming
CC host cells with a recombinant DNA having a sequence antisense to the
CC phospholipase D gene which generates mRNA which prevents the expression
CC of phospholipase D gene by hybridizing with the phospholipase D mRNA
CC from the host cell, and expressing the antisense gene in the host cells.
CC The present sequence encodes phospholipase D, which was isolated from
CC rice. Changing the composition of phospholipids produced by host cells,
CC produces phospholipids of better usability than natural phospholipids,
CC applicable in food, medicine.
XX
SQ Sequence 3040 BP; 784 A; 724 C; 783 G; 749 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 39; DB 18; Length 3040;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 576 AGTTGTGAGGGGATTGAGACACTGTGGTTCGCA 614
Db 288 AGTTGTGAGGGGATTGAGACACTGTGGTTCGCA 326

RESULT 8
AA086784
ID AA086784 standard; cDNA to mRNA; 2708 BP.
XX
AC AA086784;
XX
DT 04-MAR-1996 (first entry)
XX
DE DNA encoding Phospholipase D.
XX
KW phospholipase D; measurement; reagent; phospholipid level; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 107..2449
FT /tag=a
FT /product= phospholipase D
XX
FN WO9509234-A1.
XX
PD 06-APR-1995.
XX
PF 30-SEP-1994; 94WO-JP01627.
XX
PR 30-SEP-1993; 93JP-0267884.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Morioka S, Ueki J;
XX
DR WPI; 1995-147433/19.
DR P-PSDB; AAR12798.
XX
PT Cloned DNA coding plant derived phospholipase D - controls
PT expression of plant derived PLD gene
XX
PS Claim 9; Page 23-29; 41pp; Japanese.
XX
CC The DNA encodes a plant derived phospholipase D (PLD). The PLD is
CC useful for measuring phospholipid levels and for producing derivs.
CC by e.g. base exchange reactions. DNA controlling the expression of
CC the plant derived PLD is also claimed and shown in AA086785.
XX
SQ Sequence 2708 BP; 636 A; 709 C; 774 G; 589 T; 0 other;

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Query Match
Best Local Similarity 3.7%; Score 23; DB 16; Length 2708;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GGGCCCCCAAGTTCATCCGCAAG 37
Db 192 GGGCCCCCAAGTTCATCCGCAAG 214

RESULT 9
AB119474/C
ID AB119474 standard; DNA; 2970 BP.
XX
AC AB119474;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9895.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN W0200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-UTL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 9895; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB57737-AB572072).
XX
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2970 BP; 998 A; 540 C; 566 G; 866 T; 0 other;

Query Match
Best Local Similarity 3.4%; Score 21; DB 23; Length 2970;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 CTAAACTGAATTTATTTA 372
Db 2670 CTAAACTGAATTTATTTA 2650

RESULT 10
ABL30136/C
ID ABL30136 standard; DNA; 7862 BP.
XX

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XX PD 26-JUL-2001.  
 XX XX  
 XX PF 26-DEC-2000; 2000WO-US34263.  
 XX XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX XX  
 PA (HYSE-) HYSEQ INC.  
 XX XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX XX  
 DR WPI; 2001-442253/47.  
 DR P-PSDB; AAM42203.  
 XX XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX XX  
 PS Claim 1; SEQ ID NO 5348; 10078bp; English.  
 XX XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
 CC immunosuppressant and cyostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC assays for receptor activity, cancer diagnosis and therapy, drug screening,  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX XX  
 SQ Sequence 2115 BP; 694 A; 415 C; 427 G; 579 T; 0 other;  
 XX XX  
 Query Match 3.3%; Score 20; DB 22; Length 2115;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 530 TCTTCTCTTGTGTTGTTCTT 549  
 Db 686 TCTTCTCTTGTGTTGTTCTT 667  
 XX XX  
 RESULT 13  
 AAX77111  
 ID AAX77111 standard; DNA; 2178 BP.  
 XX XX  
 AC AAX77111;  
 XX XX  
 DT 03-AUG-1999 (first entry)  
 XX XX  
 DE Restriction fragment GC6 NcoI/XbaI.  
 XX XX  
 KW Cellular senescence; modulator; GC6 gene; senescent gene expression;  
 KW pGC6; human; ss.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN MO925878-A2.  
 XX XX

PD 27-MAY-1999.  
 XX XX  
 XX PF 19-NOV-1998; 98WO-US34996.  
 XX XX  
 PR 19-NOV-1997; 97US-0974180.  
 XX XX  
 PA (GERO-) GERON CORP.  
 XX XX  
 PI Funk W;  
 XX XX  
 DR WPI; 1999-347496/29.  
 XX XX  
 PT New human GC6 gene, useful for identifying agents for treating  
 PT diseases and/or conditions associated with cell senescence  
 XX XX  
 PS Disclosure; Page 14; 79pp; English.  
 XX XX  
 CC The invention relates to methods for modulating and identifying cellular  
 CC senescence. Recombinant expression vectors comprising a recombinant  
 CC polynucleotide corresponding to a polynucleotide in a human GC6 gene,  
 CC useful for altering senescent gene expression. The vectors and host cells  
 CC comprising the vectors are useful for identifying agents that prevent or  
 CC modulate senescent gene expression. The polynucleotides are useful for  
 CC encoding the protein, pGC6 and nucleic acid derivatives. The proteins  
 CC encoded are useful for raising antibodies specific for pGC6, which are  
 CC useful for isolating pGC6, and for detecting cells comprising pGC6 in  
 CC complex cell mixtures. The characterization of the polynucleotides enable  
 CC the identification of therapeutic agents that identify and distinguish  
 CC between young and senescent cells. This enables treatment of aging  
 CC diseases induced or exacerbated by cellular senescence.  
 XX XX  
 SQ Sequence 2178 BP; 596 A; 473 C; 436 G; 672 T; 1 other;  
 XX XX  
 Query Match 3.3%; Score 20; DB 20; Length 2178;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 530 TCTTCTCTTGTGTTGTTCTT 549  
 Db 1932 TCTTCTCTTGTGTTGTTCTT 1951  
 XX XX  
 RESULT 14  
 AAK94314  
 ID AAK94314 standard; CDNA; 2762 BP.  
 XX XX  
 AC AAK94314;  
 XX XX  
 DT 06-NOV-2001 (first entry)  
 XX XX  
 DE Human full-length CDNA, SEQ ID NO: 2985.  
 XX XX  
 KW Human; full length cDNA; CDNA synthesis; oligo-capping; ss.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN EP1130094-A2.  
 XX XX  
 PD 05-SEP-2001.  
 XX XX  
 PF 07-JUL-2000; 2000EP-0114089.  
 XX XX  
 PR 08-JUL-1999; 99JP-0194486.  
 PR 11-JAN-2000; 2000JP-0118774.  
 PR 02-MAY-2000; 2000JP-0183765.  
 XX XX  
 PA (HELT-) HELIX RES INST.  
 XX XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Iehi S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX XX  
 DR WPI; 2001-524255/58.  
 DR P-PSDB; AAM93393.  
 XX XX

XX 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX  
 PS Claim 8; SEQ ID NO 2985; 1380bp + sequence listing; English.  
 XX  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5' - and 3' - ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a full length  
 CC human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 XX  
 SQ Sequence 2762 BP; 760 A; 586 C; 569 G; 847 T; 0 other;  
 XX  
 Query Match 3.3%; Score 20; DB 22; Length 2762;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 530 TCTTCTTCTTTGTTGTTCTT 549  
 Db 2087 TCTTCTTCTTTGTTGTTCTT 2106  
 XX  
 RESULT 15  
 AAX77114  
 ID AAX77114 standard; DNA; 2970 BP.  
 XX  
 AC AAX77114;  
 XX  
 DT 03-AUG-1999 (first entry)  
 XX  
 DE DNA sequence of GC6 gene.  
 XX  
 KM Cellular senescence; modulator; GC6 gene; senescent gene expression;  
 KM pGC6; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO925878-A2.  
 XX  
 PD 27-MAY-1999.  
 XX  
 PF 19-NOV-1998; 98MO-US24996.  
 XX  
 PR 19-NOV-1997; 97US-0974180.  
 XX  
 PA (GERO-) GERON CORP.  
 XX  
 PI Funk W;  
 XX  
 DR WPI: 1999-347496/29.  
 DR P-PsDB; AAY21556.  
 XX  
 PT New human GC6 gene, useful for identifying agents for treating  
 PT diseases and/or conditions associated with cell senescence  
 XX  
 PS Claim 1; Page 15-17; 79pp; English.  
 XX  
 CC The invention relates to methods for modulating and identifying cellular  
 CC senescence. Recombinant expression vectors comprising a recombinant  
 CC polynucleotide corresponding to a polynucleotide in a human GC6 gene, are  
 CC useful for altering senescent gene expression. The vectors and host cells  
 CC comprising the vectors are useful for identifying agents that prevent or  
 CC modulate senescent gene expression. The polynucleotides are useful for  
 CC producing the protein, pGC6 and nucleic acid derivatives. The proteins  
 CC encoded are useful for raising antibodies specific for pGC6, which are

CC useful for isolating pGC6, and for detecting cells comprising pGC6 in  
 CC complex cell mixtures. The characterization of the polynucleotides enable  
 CC the identification of therapeutic agents that identify and distinguish  
 CC between young and senescent cells. This enables treatment of aging  
 CC diseases induced or exacerbated by cellular senescence.  
 XX  
 SQ Sequence 2970 BP; 829 A; 623 C; 586 G; 931 T; 1 other;  
 XX  
 Query Match 3.3%; Score 20; DB 20; Length 2970;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 2290 TCTTCTTCTTTGTTGTTCTT 2309  
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 Search completed: April 3, 2003, 11:49:57  
 Job time : 252 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 11:50:03 ; Search time 47 Seconds  
(without alignments)  
4006.373 Million cell updates/sec

Title: US-09-856-725-2

Perfect score: 614

Sequence: 1 ccgcgcacagcggagcgcgc.....ggacactgtcgttcgcgca 614

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 1533381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Issued Patents NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the chance being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	39	6.4	3040	1 US-08-446-794A-1	Sequence 1, Appl1
4	39	6.4	3040	1 US-08-750-007-2	Sequence 2, Appl1
5	39	6.4	3040	2 US-08-945-024-1	Sequence 1, Appl1
6	23	3.7	2804	1 US-08-446-794A-3	Sequence 3, Appl1
7	20	3.3	2178	3 US-08-974-180-11	Sequence 11, Appl1
8	20	3.3	2970	3 US-08-974-180-14	Sequence 14, Appl1
9	18	2.9	139	3 US-08-952-973-17	Sequence 17, Appl1
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## ALIGNMENTS

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RESULT 1
US-08-446-794A-5
; Sequence 5, Application US/08446794A
; Patent No. 5747327
; GENERAL INFORMATION:
; APPLICANT: UEKI, JUN
; APPLICANT: MORIOKA, SHINJI
; TITLE OF INVENTION: PHOSPHOLIPASE D GENE ORIGINATED FROM
; TITLE OF INVENTION: PLANT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,794A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0760-0203P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1876..1983
; FEATURE:
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NAME/KEY: CDS
LOCATION: 2524..2799
US-08-446-794A-5
Query Match 100.0%; Score 614; DB 1; Length 2799;
Best Local Similarity 100.0%; Pred. No. 2,5e+289;
Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1947 CCGGCCAGCGGAAGCGCCCAAGTTCATCCGGAAGTTGAGACCTTCTCTTAATCT 2006
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US-08-750-007-4
; Sequence 4, Application US/08750007
; Patent No. 5801016
; GENERAL INFORMATION:
; APPLICANT: MORIOKA, SHINJI
; APPLICANT: UEKI, JUN
; TITLE OF INVENTION: DNA FRAGMENT, RECOMBINANT VECTOR
; TITLE OF INVENTION: CONTAINING THE SAME AND METHOD FOR EXPRESSING FOREIGN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,007
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-221P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2799 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1876..1983
NAME/KEY: CDS
LOCATION: 2524..2799
US-08-750-007-4
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Query Match 100.0%; Score 614; DB 1; Length 2799;

Best Local Similarity 100.0%; Pred. No. 2.5e-289; Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ACTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
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## RESULT 3

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US-08-446-794A-1
Sequence 1, Application US/08446794A
Patent No. 5747327
GENERAL INFORMATION:
APPLICANT: UEXI, JUN
TITLE OF INVENTION: PHOSPHOLIPASE D GENE ORIGINATED FROM
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,794A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-0203P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 182..2617
US-08-446-794A-1
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Query Match 6.4%; Score 39; DB 1; Length 3040;

Best Local Similarity 100.0%; Pred. No. 7.3e-10; Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 288 AGTTTGAGAGGGATTGAGACACTGTGGGTGCGCA 326
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## RESULT 4

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US-08-750-007-2
Sequence 2, Application US/08750007
Patent No. 5801016
GENERAL INFORMATION:
APPLICANT: MORIOKA, SHINJI
APPLICANT: UEXI, JUN
TITLE OF INVENTION: DNA FRAGMENT, RECOMBINANT VECTOR
TITLE OF INVENTION: CONTAINING THE SAME AND METHOD FOR EXPRESSING FOREIGN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
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STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,007
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 182..2617
US-08-750-007-2

Query Match
Best Local Similarity 6.4%; Score 39; DB 1; Length 3040;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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Sequence 1, Application US/08945024
Patent No. 5973226
GENERAL INFORMATION:
APPLICANT: Ueki, Jun
APPLICANT: MORIOKA, SHINJI
TITLE OF INVENTION: METHOD FOR CHANGING COMPOSITION OF
TITLE OF INVENTION: PHOSPHOLIPIDS PRODUCED BY ORGANISM AND RECOMBINANT VECTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,024
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2804 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..2542
US-08-446-794A-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3040 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 182..2617
US-08-945-024-1

Query Match
Best Local Similarity 6.4%; Score 39; DB 2; Length 3040;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 AGTTGTGAGGGGATTGAGACACTGTGGTGGCA 614
DB 288 AGTTGTGAGGGGATTGAGACACTGTGGTGGCA 326

RESULT 6
US-08-446-794A-3
Sequence 3, Application US/08446794A
Patent No. 5747327
GENERAL INFORMATION:
APPLICANT: Ueki, Jun
APPLICANT: MORIOKA, SHINJI
TITLE OF INVENTION: PHOSPHOLIPASE D GENE ORIGINATED FROM
TITLE OF INVENTION: PLANT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,794A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2804 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..2542
US-08-446-794A-3

Query Match
Best Local Similarity 3.7%; Score 23; DB 1; Length 2804;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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APPLICATION NUMBER: US/08/952,973  
FILING DATE: 06-JAN-1998  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/IB96/00562  
FILING DATE: 06-JUN-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: EP 95401322.3  
FILING DATE: 08-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Granados, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 065691/0129  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-952-973-17

Query Match 2.9%; Score 18; DB 3; Length 139;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 308 TGTGTGATGTGTGTGTGTG 325  
Db 86 TGTGTGATGTGTGTGTGTG 69

RESULT 10  
US-09-641-638-458/c  
Sequence 458, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GENSET.051CP1  
CURRENT APPLICATION NUMBER: US/09/641,638  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 458  
LENGTH: 1001  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 501  
OTHER INFORMATION: 12-310-105 : polymorphic base G or C  
NAME/KEY: misc binding  
LOCATION: 481..500  
OTHER INFORMATION: 12-310-105.misl, potential  
NAME/KEY: misc binding  
LOCATION: 502..521  
OTHER INFORMATION: 12-310-105.mis2, potential complement

NAME/KEY: primer bind  
LOCATION: 397..415  
OTHER INFORMATION: upstream amplification primer  
NAME/KEY: primer bind  
LOCATION: 826..845  
OTHER INFORMATION: downstream amplification primer, complement  
LOCATION: 489..513  
OTHER INFORMATION: 12-310-105 potential probe  
US-09-641-638-458

Query Match 2.9%; Score 18; DB 4; Length 1001;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 453 TTTATTATTATTATTACT 470  
Db 265 TTTATTATTATTATTACT 248

RESULT 11  
US-08-973-462-1  
Sequence 1, Application US/08973462B  
Patent No. 6191270  
GENERAL INFORMATION:  
APPLICANT: DRULHE, PIERRE  
APPLICANT: DAUBERSIES, PIERRE  
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES  
FILE REFERENCE: 0660-0125-0 PCT  
CURRENT APPLICATION NUMBER: US/08/973,462B  
PRIOR FILING DATE: 1998-02-06  
EARLIER APPLICATION NUMBER: PCT/FR96/00894  
EARLIER FILING DATE: 1996-06-12  
EARLIER APPLICATION NUMBER: FR 95/07007  
EARLIER FILING DATE: 1995-06-13  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 6152  
TYPE: DNA  
ORGANISM: P. falciparum  
US-08-973-462-1

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Best Local Similarity 100.0%; Pred. No. 11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 TTTTATTATTATTATA 468  
Db 397 TTTTATTATTATTATA 414

RESULT 12  
US-09-078-294-4/c  
Sequence 4, Application US/09078294  
Patent No. 6265211  
GENERAL INFORMATION:  
APPLICANT: Choo, Kong-Hong Andy  
APPLICANT: Du Sart, Desiree  
APPLICANT: Cancilla, Michael R.  
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE  
FILE REFERENCE: Davies Col  
CURRENT APPLICATION NUMBER: US/09/078,294  
PRIOR FILING DATE: 1998-05-13  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 80246  
TYPE: DNA  
ORGANISM: Nucleotide sequence of NC-contig  
US-09-078-294-4

Query Match 2.9%; Score 18; DB 4; Length 80246;



Best Local Similarity 100.0%; Pred. No. 11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 451 TTTTATTATTATTAA 468  
Db 33054 TTTTATTATTATTAA 33037

RESULT 13  
US-09-078-294-3/c  
; Sequence 3, Application US/09078294  
; Patent No. 6265211  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Kong-Hong Andy  
; APPLICANT: Du Sart, Desiree  
; APPLICANT: Cancilla, Michael R.  
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE  
; FILE REFERENCE: Davies Col  
; CURRENT APPLICATION NUMBER: US/09/078,294  
; CURRENT FILING DATE: 1998-05-13  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patent Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 80595  
; TYPE: DNA  
; ORGANISM: Nucleotide sequence of HC-contig  
US-09-078-294-3

Query Match 2.9%; Score 18; DB 4; Length 80595;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 TTTTATTATTATTAA 468  
Db 33307 TTTTATTATTATTAA 33290

RESULT 14  
US-08-623-906A-16  
; Sequence 16, Application US/08623906A  
; Patent No. 5874217  
; GENERAL INFORMATION:  
; APPLICANT: Stevenson, Tamara  
; APPLICANT: Dvorak, Jan  
; APPLICANT: Halverson, Joy  
; TITLE OF INVENTION: Microsatellite Sequences for Canine  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; City: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/623,906A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sherwood, Pamela J.  
; REGISTRATION NUMBER: 36,677  
; TELEPHONE/DOCKET NUMBER: A-62282/BIR  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 251 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1..131  
; OTHER INFORMATION: /note= "Nucleotides 1-131 are  
; OTHER INFORMATION: unique flanking sequence"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 132..186  
; OTHER INFORMATION: /note= "Nucleotides 132-186 are  
; OTHER INFORMATION: repeat sequence"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 187..251  
; OTHER INFORMATION: /note= "Nucleotides 187-251 are  
; OTHER INFORMATION: unique flanking sequence"  
US-08-623-906A-16

Query Match 2.8%; Score 17; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 GTTTTATTATTATT 466  
Db 129 GTTTTATTATTATT 145

RESULT 15  
US-09-328-111-329/c  
; Sequence 329, Application US/09328111  
; Patent No. 6262333  
; GENERAL INFORMATION:  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Steinmann, Kathleen E.  
; APPLICANT: Astle, Jon H.  
; APPLICANT: Burgess, Christopher C.  
; APPLICANT: Bushnell, Steven E.  
; APPLICANT: Carroll III, Eddie  
; APPLICANT: Catino, Theodore J.  
; APPLICANT: Dertl, Adnan  
; APPLICANT: Ford, Donna M.  
; APPLICANT: Lewis, Marcia E.  
; APPLICANT: Monahan, John E.  
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
; FILE REFERENCE: CCD-257 (US)  
; CURRENT APPLICATION NUMBER: US/09/328,111  
; CURRENT FILING DATE: 1999-06-08  
; EARLIER APPLICATION NUMBER: US 60/088,801  
; EARLIER FILING DATE: 1998-06-10  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PaestSeq for Windows Version 3.0  
; SEQ ID NO 329  
; LENGTH: 467  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(467)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-328-111-329

Query Match 2.8%; Score 17; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 453 TTTTATTATTATTAA 469  
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Fri Apr 4 08:49:33 2003

us-09-856-725-2.oligo.rni

Page 14

Db 365 TTATTATTATTATAC 349

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Job time : 130 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 12:34:25 ; Search time 87 Seconds  
(without alignments)  
6190.586 Million cell updates/sec

Title: US-09-856-725-2

Perfect score: 614  
Sequence: 1 ccgcgcacagcggaagcgccc.....ggacactcgtcgtcgcgca 614

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 593429 seqs, 438583890 residues

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Minimum DB seq length: 0

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Published Applications\_NA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	23	3.7	2997	9 US-10-078-770-125	Sequence 125, App
2	20	3.3	2000	9 US-09-938-842A-5092	Sequence 5092, App
3	19	3.1	302	10 US-09-969-373-413	Sequence 413, App
4	19	3.1	302	10 US-09-969-373-417	Sequence 417, App
5	19	3.1	1288	9 US-09-938-842A-4207	Sequence 4207, App
6	19	3.1	1305	9 US-09-822-846-20	Sequence 20, Appl
7	19	3.1	2000	9 US-09-938-842A-4381	Sequence 4381, App
8	19	3.1	249487	9 US-10-026-188-3	Sequence 3, Appl1
9	18	2.9	117	10 US-09-969-373-1357	Sequence 1357, App
10	18	2.9	131	10 US-09-969-373-1077	Sequence 1077, App
11	18	2.9	140	10 US-09-969-373-387	Sequence 387, App
12	18	2.9	145	10 US-09-969-373-422	Sequence 422, App
13	18	2.9	145	10 US-09-969-373-517	Sequence 517, App
14	18	2.9	246	10 US-09-923-876-2923	Sequence 2923, App
15	18	2.9	284	10 US-09-969-373-616	Sequence 616, App
16	18	2.9	284	10 US-09-969-373-617	Sequence 617, App
17	18	2.9	306	10 US-09-969-373-1187	Sequence 1187, App
18	18	2.9	417	10 US-09-960-352-12649	Sequence 12649, A
19	18	2.9	1301	9 US-09-938-842A-2724	Sequence 2724, App

20	18	2.9	1500	10 US-09-974-300-172	Sequence 172, App
21	18	2.9	1923	9 US-09-938-842A-3051	Sequence 3051, App
22	18	2.9	2000	9 US-09-938-842A-4103	Sequence 4103, App
23	18	2.9	6152	9 US-09-742-096-1	Sequence 1, Appl1
24	18	2.9	11185	10 US-09-764-860-1096	Sequence 1096, App
25	18	2.9	21358	9 US-09-764-872-816	Sequence 816, App
26	18	2.9	21676	9 US-09-764-872-815	Sequence 815, App
27	18	2.9	23603	9 US-09-860-670-264	Sequence 264, App
28	18	2.9	23613	9 US-09-860-670-258	Sequence 258, App
29	18	2.9	24218	9 US-09-860-670-263	Sequence 263, App
30	18	2.9	32190	9 US-09-860-670-255	Sequence 255, App
31	18	2.9	32249	9 US-09-860-670-260	Sequence 260, App
32	18	2.9	126512	10 US-09-804-474A-3	Sequence 3, Appl1
33	18	2.9	170834	10 US-09-835-232-7	Sequence 314, Appl1
34	18	2.9	174424	10 US-09-967-768A-114	Sequence 73, Appl1
35	17	2.8	96	10 US-09-969-373-73	Sequence 39, Appl1
36	17	2.8	107	10 US-09-969-373-39	Sequence 1392, App
37	17	2.8	148	10 US-09-969-373-1392	Sequence 1442, App
38	17	2.8	148	10 US-09-969-373-1442	Sequence 1179, App
39	17	2.8	149	10 US-09-969-373-1179	Sequence 988, App
40	17	2.8	178	10 US-09-969-373-988	Sequence 989, App
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43	17	2.8	223	10 US-09-969-373-1531	Sequence 1531, App
44	17	2.8	239	10 US-09-969-373-1295	Sequence 1295, App
45	17	2.8	262	10 US-09-728-446-422	Sequence 422, App
46	17	2.8	275	10 US-09-954-456-1702	Sequence 1702, App
47	17	2.8	441	9 US-10-025-380-637	Sequence 637, App
48	17	2.8	441	10 US-09-922-217-637	Sequence 637, App
49	17	2.8	441	10 US-09-833-263-637	Sequence 637, App
50	17	2.8	456	10 US-09-770-444-533	Sequence 533, App
51	17	2.8	467	10 US-09-879-536-339	Sequence 329, App
52	17	2.8	471	10 US-09-770-444-172	Sequence 172, App
53	17	2.8	471	10 US-09-924-035A-225	Sequence 225, App
54	17	2.8	492	10 US-09-867-701-7161	Sequence 7161, App
55	17	2.8	498	10 US-09-925-300-781	Sequence 781, App
56	17	2.8	507	10 US-09-867-701-4003	Sequence 4003, App
57	17	2.8	557	9 US-10-046-935-525	Sequence 525, App
58	17	2.8	557	9 US-09-878-178-525	Sequence 525, App
59	17	2.8	582	10 US-09-864-761-15412	Sequence 15412, A
60	17	2.8	602	10 US-09-770-149-952	Sequence 952, App
61	17	2.8	618	9 US-10-125-540-547	Sequence 547, App
62	17	2.8	618	10 US-09-764-870-547	Sequence 547, App
63	17	2.8	660	10 US-09-917-800A-1026	Sequence 1026, App
64	17	2.8	752	9 US-09-776-724A-22	Sequence 22, Appl1
65	17	2.8	1158	10 US-09-778-844-160	Sequence 160, App
66	17	2.8	1297	9 US-09-992-598-224	Sequence 224, App
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68	17	2.8	1297	9 US-09-989-293A-224	Sequence 224, App
69	17	2.8	1297	9 US-09-989-735-224	Sequence 224, App
70	17	2.8	1297	9 US-09-990-444-224	Sequence 224, App
71	17	2.8	1297	9 US-09-989-730-224	Sequence 224, App
72	17	2.8	1297	9 US-09-990-436-224	Sequence 224, App
73	17	2.8	1297	9 US-09-991-181-224	Sequence 224, App
74	17	2.8	1297	9 US-09-993-687-224	Sequence 224, App
75	17	2.8	1297	9 US-09-989-734-224	Sequence 224, App
76	17	2.8	1297	9 US-09-993-687-224	Sequence 224, App
77	17	2.8	1297	9 US-10-028-072-435	Sequence 435, App
78	17	2.8	1297	9 US-09-997-653-224	Sequence 224, App
79	17	2.8	1297	9 US-10-174-590-599	Sequence 599, App
80	17	2.8	1297	9 US-10-176-758-599	Sequence 599, App
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86	17	2.8	1297	9 US-10-175-738-599	Sequence 599, App
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88	17	2.8	1297	9 US-10-176-482-599	Sequence 599, App
89	17	2.8	1297	9 US-10-176-482-599	Sequence 599, App
90	17	2.8	1297	9 US-10-176-913-599	Sequence 599, App
91	17	2.8	1297	9 US-10-180-552-599	Sequence 599, App
92	17	2.8	1297	9 US-10-180-557-599	Sequence 599, App













C 823	16	2.6	1977	9	US-10-199-311-503	Sequence 503, App	C 896	16	2.6	2000	9	US-09-938-842A-5007	Sequence 5007, Ap
C 824	16	2.6	1977	9	US-10-199-314-503	Sequence 503, App	C 897	16	2.6	2000	9	US-09-938-842A-5032	Sequence 5032, Ap
C 825	16	2.6	1977	9	US-10-199-317-503	Sequence 503, App	C 898	16	2.6	2000	10	US-09-887-576-339	Sequence 339, App
C 826	16	2.6	1977	9	US-10-199-665-503	Sequence 503, App	C 899	16	2.6	2078	10	US-09-969-852-6	Sequence 6, App1
C 827	16	2.6	1977	9	US-10-199-666-503	Sequence 503, App	C 900	16	2.6	2237	9	US-10-017-910-3	Sequence 3, App1
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C 834	16	2.6	1977	9	US-10-202-470-503	Sequence 503, App	C 907	16	2.6	2456	9	US-09-822-846-42	Sequence 42, App1
C 835	16	2.6	1977	9	US-10-202-476-503	Sequence 503, App	C 908	16	2.6	2461	9	US-09-925-299-129	Sequence 129, App
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C 892	16	2.6	2000	9	US-09-938-842A-4370	Sequence 4370, Ap	C 965	16	2.6	2478	9	US-10-180-554-107	Sequence 107, App
C 893	16	2.6	2000	9	US-09-938-842A-4412	Sequence 4412, Ap	C 966	16	2.6	2478	9	US-10-180-555-107	Sequence 107, App
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## ALIGNMENTS

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RESULT 1
US-10-078-770-125
; Sequence 125, Application us/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078.770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 125
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Trifolium aestivum
US-10-078-770-125
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Query Match 3.7%; Score 23; DB 9; Length 2997;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 15 GCGCCCCCAAGTTCATCCGCAAG 37
DB 216 GCGCCCCCAAGTTCATCCGCAAG 238
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RESULT 2
US-09-938-842A-5092/c
; Sequence 5092, Application US/09938842A
; Patent No. US20020160378B1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 5092
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5092
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 714 AGAGTTTATTATTATTATT 695
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RESULT 3
US-09-969-373-413/c
; Sequence 413, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Eferetz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 413
; LENGTH: 302
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-413
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Query Match 3.1%; Score 19; DB 10; Length 302;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 452 TTTATTATTATTACT 470  
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Db 113 TTTATTATTATTACT 95

## RESULT 4

US-09-969-373-417/C  
; Sequence 417, Application US/09969373  
; Patent No. US2002013852A1  
; GENERAL INFORMATION:  
; APPLICANT: Efferetz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 417  
; LENGTH: 302  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-417

Query Match 3.1%; Score 19; DB 10; Length 302;  
Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 452 TTTATTATTATTACT 470  
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Db 113 TTTATTATTATTACT 95

## RESULT 5

US-09-938-842A-4207  
; Sequence 4207, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCLIP1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 4207  
; LENGTH: 1288  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-4207

Query Match 3.1%; Score 19; DB 9; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 8.6;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 TGTGTGATGTGTGTGTGT 326  
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Db 44 TGTGTGATGTGTGTGTGT 62

## RESULT 6

US-09-822-846-20/C  
; Sequence 20, Application US/09822846  
; Publication No. US20030027139A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: Lavallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steinhinger II, Robert J.  
; APPLICANT: Bowman, Michael R.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fectel, Kim  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakara  
; APPLICANT: Graham, James R.  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6400  
; CURRENT APPLICATION NUMBER: US/09/822,846  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/195,605  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1305  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-822-846-20

Query Match 3.1%; Score 19; DB 9; Length 1305;  
Best Local Similarity 100.0%; Pred. No. 8.7;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 CTCCTGCTCTTTCTTTT 90  
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Db 868 CTCCTGCTCTTTCTTTT 850

## RESULT 7

US-09-938-842A-4381/C  
; Sequence 4381, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCLIP1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 4381  
; LENGTH: 2000  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana

US-09-938-842A-4381

Query Match 3.1%; Score 19; DB 9; Length 2000;

Best Local Similarity 100.0%; Pred. No. 9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 448 GAGTTTATTATTATTATT 466

Db 598 GAGTTTATTATTATTATT 580

RESULT 8

US-10-026-188-3/c

; Sequence 3, Application US/10026188

; Patent No. US20020164645A1

; GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.

; APPLICANT: Zhang, Yifeng

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific

; FILE REFERENCE: 02307E-114910US

; CURRENT APPLICATION NUMBER: US/10/026,188

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: US 60/259,379

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 249487

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; OTHER INFORMATION: mouse genomic region containing ltrcps

US-10-026-188-3

Query Match 3.1%; Score 19; DB 9; Length 249487;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 ATGTGCTGTGTTTGTGT 332

Db 177388 ATGTGCTGTGTTTGTGT 177370

RESULT 9

US-09-969-373-1357/c

; Sequence 1357, Application US/09969373

; Patent No. US2002013852A1

; GENERAL INFORMATION:

; APPLICANT: Efferetz, Roger J.

; APPLICANT: Hauge, Brian M.

; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

; FILE REFERENCE: 38-10(52679)A

; CURRENT APPLICATION NUMBER: US/09/969,373

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 09/754,853

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US 09/760,427

; PRIOR FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US 09/855,768

; NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 1357

; LENGTH: 117

; TYPE: DNA

; ORGANISM: Glycine max

US-09-969-373-1357

Query Match 2.9%; Score 18; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 449 AGTTTATTATTATTATT 466

Db 60 AGTTTATTATTATTATT 43

RESULT 10

US-09-969-373-1077/c

; Sequence 1077, Application US/09969373

; Patent No. US2002013852A1

; GENERAL INFORMATION:

; APPLICANT: Efferetz, Roger J.

; APPLICANT: Hauge, Brian M.

; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

; FILE REFERENCE: 38-10(52679)A

; CURRENT APPLICATION NUMBER: US/09/969,373

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 09/754,853

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US 09/760,427

; PRIOR FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US 09/855,768

; NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 1077

; LENGTH: 131

; TYPE: DNA

; ORGANISM: Glycine max

US-09-969-373-1077

Query Match 2.9%; Score 18; DB 10; Length 131;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 449 AGTTTATTATTATTATT 466

Db 56 AGTTTATTATTATTATT 39

RESULT 11

US-09-969-373-387

; Sequence 387, Application US/09969373

; Patent No. US2002013852A1

; GENERAL INFORMATION:

; APPLICANT: Efferetz, Roger J.

; APPLICANT: Hauge, Brian M.

; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

; FILE REFERENCE: 38-10(52679)A

; CURRENT APPLICATION NUMBER: US/09/969,373

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 09/754,853

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US 09/760,427

; PRIOR FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US 09/855,768

; NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 387

; LENGTH: 140

; TYPE: DNA

; ORGANISM: Glycine max

US-09-969-373-387

Query Match 2.9%; Score 18; DB 10; Length 140;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 TTTTATTATTATTATTAA 468

Db 39 TTTTATTATTATTATTAA 56

RESULT 12

US-09-969-373-422

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; Sequence 422, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Efferetz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 422
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-422

Query Match
Best Local Similarity 2.9%; Score 18; DB 10; Length 145;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 449 AGTTTATTATTATTATT 466
DB 79 AGTTTATTATTATTATT 96
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RESULT 13
US-09-969-373-517/C
; Sequence 517, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Efferetz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 517
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-517

Query Match
Best Local Similarity 2.9%; Score 18; DB 10; Length 145;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 449 AGTTTATTATTATTATT 466
DB 67 AGTTTATTATTATTATT 50

RESULT 14
US-09-923-876-2923/C
; Sequence 2923, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Ialugudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
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; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 2923
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700161403H1
; NAME/KEY: unsure
; LOCATION: 187
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-2923

Query Match
Best Local Similarity 2.9%; Score 18; DB 10; Length 246;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 TTCTCTTTGTTGTTCTT 549
DB 145 TTCTCTTTGTTGTTCTT 128
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RESULT 15
US-09-969-373-616
; Sequence 616, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Efferetz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 616
; LENGTH: 284
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-616

Query Match
Best Local Similarity 2.9%; Score 18; DB 10; Length 284;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 GTTTTATTATTATTATTA 467
DB 56 GTTTTATTATTATTATTA 73
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Search completed: April 3, 2003, 13:36:46  
Job time : 157 secs

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 11:35:08 ; Search time 1429 Seconds

(without alignments)  
6958.733 Million cell updates/sec

Title: US-09-856-725-2

Perfect score: 614  
Sequence: 1 ccgcgcacagcggaagcgccc.....ggacactgtgggtgtcgca 614

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 809774376 residues

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Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

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- 1: em\_estba:\*
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  - 7: em\_estro:\*
  - 8: em\_hic:\*
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  - 11: gb\_hic:\*
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  - 13: gb\_est4:\*
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  - 15: em\_estfun:\*
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  - 19: em\_gss\_inv:\*
  - 20: em\_gss\_pln:\*
  - 21: em\_gss\_vrt:\*
  - 22: em\_gss\_fun:\*
  - 23: em\_gss\_man:\*
  - 24: em\_gss\_mus:\*
  - 25: em\_gss\_other:\*
  - 26: em\_gss\_pro:\*
  - 27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 2	39	6.4	447	9	AU182480 AU182480
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C 4	25	4.1	401	17	AZ919173 1006014C0
C 5	23	3.7	211	10	BE500616 WHE0987-0
C 6	23	3.7	446	10	AV922849 AV922849

7	23	3.7	480	9	A1466643
8	23	3.7	505	13	B1777193
9	23	3.7	553	10	AV926845
10	23	3.7	559	12	BF277692 GA_Eb003
11	23	3.7	581	13	Bj210608
12	23	3.7	597	10	AV924875
13	23	3.7	621	10	AV925509
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15	23	3.7	667	13	B1954591 HVSMBE001
16	23	3.7	827	12	BF617621 HVSMBE001
17	23	3.7	949	12	BG300571
18	23	3.7	974	12	BG343188
19	22	3.6	233	17	AQ09466
20	22	3.6	262	10	AM854304 RC3-CT025
21	22	3.6	483	17	AQ142239
22	22	3.6	485	17	AQ341424
23	22	3.6	1210	10	BE306852
24	21	3.4	96	17	AZ310260
25	21	3.4	244	12	BF763441
26	21	3.4	338	13	BG933460
27	21	3.4	457	13	B1246122
28	21	3.4	482	13	BG946911
29	21	3.4	509	12	BG357316
30	21	3.4	528	17	AZ474286
31	21	3.4	548	10	BE594640
32	21	3.4	642	17	CNS059PW
33	21	3.4	672	17	BH693868
34	21	3.4	683	13	B1678747
35	21	3.4	796	17	BH540689
36	21	3.4	1885	12	BG171804
37	21	3.4	2151	12	BF164231
38	20	3.3	132	10	AM421087
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42	20	3.3	342	10	AM127345
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48	20	3.3	421	17	AQ033189
49	20	3.3	424	10	AM077850
50	20	3.3	426	10	AM891768
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54	20	3.3	476	9	AL371356
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57	20	3.3	547	9	AA928115
58	20	3.3	555	17	AZ015695
59	20	3.3	556	17	DE21K205
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62	20	3.3	606	14	BQ295237
63	20	3.3	606	17	BH203252
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AV926845	AV926845	
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AV925509	AV925509	
B0739844	HB04D12 H	
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BF617621	HVSMBE001	
BG300571	HVSMBE000	
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AQ09466	GSSTC0953	
AM854304	RC3-CT025	
AQ142239	HS_3179_B	
AQ341424	RPC111-11	
BE306852	601103696	
AZ310260	1M0025G12	
BF763441	CM1-CS003	
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B1246122	IP1_67_B0	
BG946911	IP1_1_C02	
BG357316	OV2_12_D0	
AZ474286	1M0290H18	
BE594640	P11_35_G0	
AL27553	Tetraodon	
BH693868	BOMEX39TF	
B1678747	SM5585 SW	
BH540689	BOCUR83TR	
BG171804	602322574	
BF164231	601773180	
AM421087	fj91906.x	
AV224149	AV224149	
AV240701	AV240701	
AQ067518	HS_2237_B	
AM127345	ML10517_D	
AZ050396	GSSTC1124	
AZ050966	GSSTC1181	
AM208050	ML11082e	
BG731997	ps21b09.Y	
AA233672	zr43b06.Y	
AQ033189	HS_2222_A	
AM077850	fj67d03.x	
AM891768	CM3-NT008	
BF519558	EST457022	
B0122571	EST608147	
AL387091	MCBC40D02	
AL371356	MCBA43H12	
AM697472	NF099B12S	
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AA928115	om08412.s	
AZ015695	RPC1-23-3	
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BH728029	BOMLE48TF	
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BE941548	EST421118	
AZ992614	2M027701H	
AQ320446	RPC111-98	
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BQ148225	NF065A10P	
AZ631483	1M0485L08	
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C 82	20	3.3	901	17	CNS02RE1	AT210466	155	19	3.1	533	14	BQ488964
C 83	20	3.3	903	17	AL524131	AL224131	156	19	3.1	542	17	AQ456724
C 84	20	3.3	933	17	BH148832	ENTFM57TR	157	19	3.1	546	17	A2778695
C 85	20	3.3	948	13	B1093477	BG2859672	158	19	3.1	547	10	BE474837
C 86	20	3.3	949	12	BQ488976	602535015	159	19	3.1	549	10	BES50091
C 87	20	3.3	986	12	BF213231	601844716	160	19	3.1	552	12	BG086582
C 88	20	3.3	999	12	BE973045	601651913	161	19	3.1	552	17	BG086582
C 89	20	3.3	1101	17	CNS00EKO	AL069289	162	19	3.1	557	12	TA129F09Q
C 90	20	3.3	1143	12	BP981691	602306032	163	19	3.1	557	13	BF999512
C 91	20	3.3	1210	17	BF767943	BF767943	164	19	3.1	557	17	B1516515
C 92	20	3.3	1215	17	AG126235	AG126235	165	19	3.1	560	10	AM819648
C 93	20	3.3	1310	13	B1226385	602951002	166	19	3.1	579	17	AZ104263
C 94	20	3.3	1800	12	BF579071	602096001	167	19	3.1	580	12	BE138958
C 95	19	3.1	117	10	BE183294	BE183294	168	19	3.1	584	14	BQ240360
C 96	19	3.1	107	10	AL829840	AL829840	169	19	3.1	591	17	AZ367773
C 97	19	3.1	211	12	BF281730	BF281730	170	19	3.1	600	13	B177891
C 98	19	3.1	240	10	AU072820	AU072820	171	19	3.1	601	17	A2849123
C 99	19	3.1	242	10	AV799694	AV799694	172	19	3.1	603	14	BQ366739
C 100	19	3.1	256	9	AL215968	AL215968	173	19	3.1	609	14	BM949588
C 101	19	3.1	261	14	BP027055	BP027055	174	19	3.1	612	17	A2496644
C 102	19	3.1	284	10	BB330890	BB330890	175	19	3.1	615	17	A2496644
C 103	19	3.1	291	10	BB444012	BB444012	176	19	3.1	620	10	BE21897
C 104	19	3.1	292	10	AV235830	AV235830	177	19	3.1	632	13	BM013483
C 105	19	3.1	296	9	AL603292	AL603292	178	19	3.1	634	12	BF069979
C 106	19	3.1	300	10	AM408973	AM408973	179	19	3.1	641	17	AQ656246
C 107	19	3.1	329	17	AZ999143	AZ999143	180	19	3.1	645	10	AM977447
C 108	19	3.1	331	9	AA948427	AA948427	181	19	3.1	647	12	BF400405
C 109	19	3.1	333	12	BG667333	BG667333	182	19	3.1	650	17	BH003825
C 110	19	3.1	334	17	AI026410	AI026410	183	19	3.1	650	17	TH112E11Q
C 111	19	3.1	336	17	AQ904219	AQ904219	184	19	3.1	655	17	A2526061
C 112	19	3.1	338	9	AA395176	AA395176	185	19	3.1	662	9	AU005471
C 113	19	3.1	341	17	AQ0902958	AQ0902958	186	19	3.1	665	10	AV711424
C 114	19	3.1	345	9	AL164220	AL164220	187	19	3.1	669	9	AL508050
C 115	19	3.1	363	10	BE108595	BE108595	188	19	3.1	670	17	BH189653
C 116	19	3.1	368	9	AL431814	AL431814	189	19	3.1	672	17	AZ897361
C 117	19	3.1	368	10	BE095753	BE095753	190	19	3.1	678	17	AQ780047
C 118	19	3.1	371	10	BE095753	BE095753	191	19	3.1	685	17	A2643015
C 119	19	3.1	374	14	BQ985106	BQ985106	192	19	3.1	685	17	BH313755
C 120	19	3.1	383	14	BQ990261	BQ990261	193	19	3.1	688	17	AZ861126
C 121	19	3.1	390	9	AI434130	AI434130	194	19	3.1	699	10	BE038274
C 122	19	3.1	397	17	BH266072	BH266072	195	19	3.1	699	17	BH542334
C 123	19	3.1	398	10	BE581301	BE581301	196	19	3.1	707	14	BQ429141
C 124	19	3.1	408	9	AL719067	AL719067	197	19	3.1	715	17	AG044365
C 125	19	3.1	408	17	AZ301759	AZ301759	198	19	3.1	717	10	BES85601
C 126	19	3.1	409	14	BM699583	BM699583	199	19	3.1	719	12	BG366170
C 127	19	3.1	410	10	BE096712	BE096712	200	19	3.1	728	13	BJ137637
C 128	19	3.1	410	10	BE098668	BE098668	201	19	3.1	737	10	AV716641
C 129	19	3.1	420	17	AZ004903	AZ004903	202	19	3.1	743	17	AZ956596
C 130	19	3.1	425	12	BF416095	BF416095	203	19	3.1	749	17	BH595963
C 131	19	3.1	427	9	AA923655	AA923655	204	19	3.1	751	12	BG722964
C 132	19	3.1	429	17	BH617859	BH617859	205	19	3.1	752	13	BJ128415
C 133	19	3.1	451	9	AA858072	AA858072	206	19	3.1	764	10	AW906711
C 134	19	3.1	453	9	AI271949	AI271949	207	19	3.1	767	17	BH260906
C 135	19	3.1	461	9	AL819958	AL819958	208	19	3.1	787	9	AL692232
C 136	19	3.1	464	10	AM214337	AM214337	209	19	3.1	800	17	BH479528
C 137	19	3.1	464	12	BF925205	BF925205	210	19	3.1	802	17	BH035305
C 138	19	3.1	467	10	AM136096	AM136096	211	19	3.1	802	17	BH250603
C 139	19	3.1	470	17	AO669923	AO669923	212	19	3.1	813	17	BH442900
C 140	19	3.1	475	14	BO174737	BO174737	213	19	3.1	822	17	CNS011WB
C 141	19	3.1	478	9	AA767888	AA767888	214	19	3.1	835	17	AZ671021
C 142	19	3.1	478	12	BF994060	BF994060	215	19	3.1	840	9	AU136903
C 143	19	3.1	481	12	BF414475	BF414475	216	19	3.1	850	17	BH348288
C 144	19	3.1	491	13	BF13681	BF13681	217	19	3.1	878	17	AZ681716
C 145	19	3.1	491	13	BI780884	BI780884	218	19	3.1	892	14	BQ231024
C 146	19	3.1	497	17	AO124210	AO124210	219	19	3.1			
C 147	19	3.1	498	9	AI679779	AI679779	220	19	3.1			
C 148	19	3.1	505	13	BI313695	BI313695	221	19	3.1			
C 149	19	3.1	508	12	BF471629	BF471629	222	19	3.1			
C 150	19	3.1	509	9	AL826553	AL826553	223	19	3.1			
C 151	19	3.1	509	17	AO403594	AO403594	224	19	3.1			
C 152	19	3.1	521	9	AF155012	AF155012	225	19	3.1			













C 956	17	2.8	139	17	A2766308	A2766308	1M0563118
957	17	2.8	140	9	AU269864	AU269864	AU269864
958	17	2.8	141	9	AU262105	AU262105	AU262105
959	17	2.8	144	9	A1577428	UI-R-AU01	A1577428
C 960	17	2.8	147	12	BF876508	IL3-ET011	BF876508
C 961	17	2.8	148	10	AV643398	AV643398	AV643398
C 962	17	2.8	148	13	BJ339549	BJ339549	BJ339549
C 963	17	2.8	153	12	BQ106311	602289671	BQ106311
C 964	17	2.8	153	13	BJ369604	BJ369604	BJ369604
C 965	17	2.8	154	9	AA275254	VC02F10 r	AA275254
C 966	17	2.8	154	10	AM935520	RC2-DT000	AM935520
C 967	17	2.8	154	17	BH040587	RPCT-24-3	BH040587
C 968	17	2.8	155	17	AZ059578	RPCT-23-4	AZ059578
C 970	17	2.8	156	9	AA437909	VD22H02.S	AA437909
C 971	17	2.8	161	9	AU262586	AU262586	AU262586
C 972	17	2.8	163	13	BJ335267	BJ335267	BJ335267
C 973	17	2.8	164	12	BF356700	QV2-NT004	BF356700
C 974	17	2.8	164	17	AL768469	Arabidops	AL768469
C 975	17	2.8	165	10	BB588561	BB588561	BB588561
C 976	17	2.8	169	10	AM849258	IL3-CT021	AM849258
C 977	17	2.8	169	14	AM849453	IL3-CT021	AM849453
C 978	17	2.8	172	10	AM882063	MR2-OT004	AM882063
C 979	17	2.8	172	17	AZ029644	RPCT-23-3	AZ029644
C 980	17	2.8	174	14	C91520	C91520	C91520
C 981	17	2.8	175	17	AZ269932	RPCT-23-1	AZ269932
C 982	17	2.8	176	10	BB035400	BB035400	BB035400
C 983	17	2.8	176	16	B1452062	G104 A09	B1452062
C 984	17	2.8	176	14	BU017295	BU017295	OHE15H01
C 985	17	2.8	177	9	AU259853	AU259853	AU259853
C 986	17	2.8	177	12	BE897708	601439243	BE897708
C 987	17	2.8	179	13	BJ339385	BJ339385	BJ339385
C 988	17	2.8	179	13	BU343024	BU343024	BU343024
C 989	17	2.8	180	9	AV287799	AV287799	AV287799
C 990	17	2.8	184	13	B1189825	G2A11f5.F	B1189825
C 991	17	2.8	187	9	AU054008	AU054008	AU054008
C 992	17	2.8	187	10	BE151771	QVO-HT030	BE151771
C 993	17	2.8	189	17	AZ734630	RPCT-24-1	AZ734630
C 994	17	2.8	190	9	AQ140860	HS 3123 A	AQ140860
C 995	17	2.8	191	9	AA516254	ng66d06.F	AA516254
C 996	17	2.8	191	13	BJ338593	BJ338593	BJ338593
C 997	17	2.8	191	14	N71440	2a38h08.81	N71440
C 998	17	2.8	192	12	BE937028	PM3-SN002	BE937028
C 999	17	2.8	192	13	BM137527	WHE0483-0	BM137527
C1000	17	2.8	193	14	C90663	C90663	D1CT

## ALIGNMENTS

RESULT 1  
A0576571/c 560 bp DNA linear GSS 02-JUN-1999  
LOCUS A0576571.1 GI:4977056  
DEFINITION nbx0089K24f CUGI Rice BAC Library Oryza sativa genomic clone  
ACCESSION A0576571.1  
VERSION A0576571.1  
KEYWORDS GSS.  
SOURCE Oryza sativa.  
ORGANISM Oryza sativa.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriatoidae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS Wing, R.A. and Dean, R.A.  
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome  
JOURNAL Unpublished (1998)  
COMMENT Contact: Ming RA  
Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293

FEATURES  
source  
Email: rwing@clemson.edu  
Seq primer: TATACGACCTACCTATAGG  
Class: BAC ends  
High quality sequence stop: 354.  
Location/Qualifiers  
1..560  
/organism="Oryza sativa"  
/strain="Japonica"  
/cultivar="Nipponbare"  
/db\_xref="taxon:4530"  
/clone="nbx0089K24f"  
/issue\_type="leaf"  
/issue="Vector: pBel08AC11; Site 1: HindIII; Site 2:  
/lab host="E. coli DH10B"  
/note="Rice is one of two most popular grains in the  
HindIII. Half of the world population especially those  
inhabiting highly populated areas of the humid tropics  
and subtropics, rely on rice as their primary source of  
carbohydrate. Monocotyledonous rice is a diploid plant  
(2n=24) with a haploid genome equivalent of 431 Mbp  
(Arumuganathan and Earle, 1991). The relatively small  
genome of rice, three times larger than that of  
Arabidopsis, makes it suitable for genomic studies. In  
order to facilitate positional cloning, physical mapping  
and genome sequencing of rice, we have constructed a BAC  
library from Oryza sativa, Nipponbare variety. The  
library contains 36,864 clones with an average insert size  
of 128.5 Kb providing 10.9 haploid genome equivalents. The  
deep coverage allows the isolation a particular sequence  
with a probability of 99.9%. Two high density filters,  
each containing 18,432 clones (doubly spotted), represent  
the whole library for colony screening."

## BASE COUNT

176 a 132 c 107 g 145 t

Query Match 42.3%; Score 260; DB 17; Length 560;  
Best Local Similarity 100.0%; Pred. No. 5,5e-123;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	355	AAACTGAAATTTTATTATTATTAAGTACGCTACCTAAAGTGAAGTTCCTGCTGATG	414
DB	556	AACTGAAATTTTATTATTATTAAGTACGCTACCTAAAGTGAAGTTCCTGCTGATG	497
QY	415	TGCTGCTGCTACCAAAATCTTGATTGAGATTATTTATTATTATTAAGTACG	474
DB	496	TGCTGCTGCTACCAAAATCTTGATTGAGATTATTTATTATTATTAAGTACG	437
QY	475	TACTACAAATCTATGCTGATGCTATGCTGCTGCTATACCTGAATGCAATGCTTC	534
DB	436	TACTACAAATCTATGCTGATGCTGATGCTGCTGCTGCTATACCTGAATGCAATGCTTC	377
QY	535	TTCTTTGTTGTTCTTGTATCTAAACGCTGATGCTGATGCTGATGCTGATGCTG	594
DB	376	TTCTTTGTTGTTCTTGTATCTAAACGCTGATGCTGATGCTGATGCTGATGCTG	317
QY	595	GGACACTGTGGGTGTCGCA	614
DB	316	GGACACTGTGGGTGTCGCA	297

RESULT 2  
AUI82480 447 bp mRNA linear EST 03-APR-2002  
LOCUS AUI82480  
DEFINITION Aui82480 Rice panicle at flowering stage Oryza sativa (japonica  
cultivar-group) cDNA clone E3226, mRNA sequence.  
ACCESSION AUI82480  
VERSION AUI82480.1 GI:13896144  
KEYWORDS EST.  
SOURCE Oryza sativa (japonica cultivar-group).  
ORGANISM Oryza sativa (japonica cultivar-group).  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE  
1 (bases 1 to 447)  
AUTHORS  
TITLE  
Rice cDNA from panicle at flowering stage (2001)  
JOURNAL  
COMMENT  
Contact: Takuji Sasaki  
National Institute of Agrobiological Resources  
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki  
305-8602, Japan  
Tel: 81-298-38-7441  
Fax: 81-298-38-7468  
Email: tsasaki@ab.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/  
PROJECT = 'RGP'

FEATURES  
source  
Location/Qualifiers  
1..447  
/organism="Oryza sativa (japonica cultivar-group)"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/clone="E3226"  
/clone\_lib="Rice panicle at flowering stage"  
/dev\_stage="flowering stage"  
/note="Organ: panicle; Rice cDNA from panicle at flowering stage"

BASE COUNT  
105 a 116 c 132 g 94 t

Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e-09; Length 447;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 576 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGGCA 614  
Db 154 AGTTTGTGAGGGGATTGAGACACTGTGGTGTGGCA 192

RESULT 3  
BH219271/c 153 bp DNA linear GSS 08-NOV-2001  
LOCUS  
DEFINITION  
1006085F05.x1 1006 - Rescemu Grid G Zea mays genomic, DNA  
sequence.  
ACCESSION  
BH219271 GI:16813113  
VERSION  
BH219271.1  
KEYWORDS  
GSS.  
SOURCE  
Zea mays.  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 153)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site so sequence was trimmed. Post-ligation  
sequence submitted separately.  
Plate: 1006085 row: 20  
Class: transposon-tagged.

FEATURES  
source  
Location/Qualifiers  
1..153  
/organism="Zea mays"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/clone\_lib="1006 - Rescemu Grid G"  
/clone\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: leaf; Vector: Rescemu (engineered from

ampicillin."

BASE COUNT  
30 a 28 c 75 g 20 t

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.085; Length 153;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 GCGCCCCCAAGTTCATCCGCAAGT 39  
Db 74 GCGCCCCCAAGTTCATCCGCAAGT 50

RESULT 4  
AZ919173/c 401 bp DNA linear GSS 17-DEC-2001  
LOCUS  
DEFINITION  
1006014C02.2EL\_x1 1006 - Rescemu Grid G Zea mays genomic, DNA  
sequence.  
ACCESSION  
AZ919173 GI:13388594  
VERSION  
AZ919173.1  
KEYWORDS  
GSS.  
SOURCE  
Zea mays.  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 401)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonucleases.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1006014 row: 39  
Class: transposon-tagged.

FEATURES  
source  
Location/Qualifiers  
1..401  
/organism="Zea mays"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/clone\_lib="1006 - Rescemu Grid G"  
/clone\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: leaf; Vector: Rescemu (engineered from

ampicillin. Site 1: BamHI; Site 2: BglII;  
Rescemu is a 4.9 kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescemu, go to the web  
site 'www.zmmb.iastate.edu' and follow the links for  
'Rescemu.' Grid G was grown at Stanford in 2000. DNA was  
extracted from leaf punches, double digested using BamHI  
and BglII, and ligated to form circular plasmids. DH10B  
cells were transformed and then screened on LB plates with  
ampicillin."

BASE COUNT  
105 a 75 c 144 g 77 t

## ORIGIN

Query Match 4.1%; Score 25; DB 17; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.097;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GCGCCCCAAGTTCATCCGCAAGT 39  
 Db 324 GCGCCCCAAGTTCATCCGCAAGT 300

RESULT 5 BE500616 211 bp mRNA linear EST 04-AUG-2000

LOCUS WHE0987-0990 L19 L19S2 wheat pre-anthesis spike cDNA library  
 DEFINITION Triticum aestivum cDNA clone WHE0987-0990\_L19\_L19, mRNA sequence.

ACCESSION BE500616 GI:9669233

VERSION BE500616.1  
 KEYWORDS EST.  
 SOURCE bread wheat.  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae

REFERENCE 1 (bases 1 to 211)  
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han  
 'P.S., Heia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,  
 Seaton, C.L. and Tong, J.C.  
 The structure and function of the expressed portion of the wheat  
 genomes - pre-anthesis spike cDNA library

TITLE Unpublished (2000)  
 JOURNAL Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818  
 Email: oanderson@pw.usda.gov  
 Sequence have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20  
 Seq primer: Stratagene SK primer.

FEATURES  
 source  
 Location/Qualifiers  
 1..211  
 /organism="Triticum aestivum"  
 /cultivar="Chinese Spring"  
 /db\_xref="taxon:4565"  
 /clone="WHE0987-0990\_L19\_L19"  
 /clone\_1b="wheat pre-anthesis spike cDNA library"  
 /tissue\_type="Spike before anthesis"  
 /dev\_stage="Adult plant"  
 /lab\_host="E. coli SOLA"  
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
 Site 1: EcoRI, Site 2: XhoI; plates were grown in the  
 greenhouse. Whole spike with awns trimmed, white, green  
 and yellow anther were collected and total RNA, and  
 poly(A) RNA were prepared, a cDNA library was made, and  
 the cDNA clones were in vivo excised to give pluscript  
 phagemids in the T7 Close lab (Choi, Close, Fenton) at  
 the University of California, Riverside. Plasmid DNA  
 preparations and DNA sequencing were performed in the OD  
 Anderson lab (all other authors)."

BASE COUNT 28 a 71 c 66 g 46 t  
 ORIGIN  
 Query Match 3.7%; Score 23; DB 10; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 0.96;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GCGCCCCAAGTTCATCCGCAAG 37  
 Db 178 GCGCCCCAAGTTCATCCGCAAG 200

FEATURES  
 source  
 Location/Qualifiers  
 1..446  
 /organism="Hordeum vulgare subsp. vulgare"  
 /cultivar="Haruna Nijo"  
 /db\_xref="taxon:112509"  
 /clone="basd2j19"  
 /clone\_1b="K. Sato unpublished cDNA library, cv. Haruna  
 Nijo second leaf stage seedling leaves"  
 /tissue\_type="seedling leaves"  
 /dev\_stage="second leaf stage"  
 Location/Qualifiers

RESULT 6 AV922849 446 bp mRNA linear EST 18-JAN-2002

LOCUS AV922849 K Sato unpublished cDNA library, cv. Haruna Nijo second  
 DEFINITION leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA  
 clone basd2j19 5', mRNA sequence.

ACCESSION AV922849 GI:18218628  
 VERSION AV922849.1  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare.  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae

REFERENCE 1 (bases 1 to 446)  
 Sato, K., Saito, D. and Takeda, K.  
 Barley EST sequencing project in NIG and Okayama Univ  
 Unpublished (2002)  
 Contact: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshin@genes.nig.ac.jp.

FEATURES  
 source  
 Location/Qualifiers  
 1..446  
 /organism="Hordeum vulgare subsp. vulgare"  
 /cultivar="Haruna Nijo"  
 /db\_xref="taxon:112509"  
 /clone="basd2j19"  
 /clone\_1b="K. Sato unpublished cDNA library, cv. Haruna  
 Nijo second leaf stage seedling leaves"  
 /tissue\_type="seedling leaves"  
 /dev\_stage="second leaf stage"  
 Location/Qualifiers

BASE COUNT 73 a 146 c 126 g 101 t  
 ORIGIN  
 Query Match 3.7%; Score 23; DB 10; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GCGCCCCAAGTTCATCCGCAAG 37  
 Db 211 GCGCCCCAAGTTCATCCGCAAG 233

FEATURES  
 source  
 Location/Qualifiers  
 1..480  
 /organism="Hordeum vulgare"  
 /db\_xref="taxon:4513"

RESULT 7 AV466643 480 bp mRNA linear EST 24-MAY-2002

LOCUS AV466643  
 DEFINITION Hordeum vulgare cDNA clone S0000800211A09F1, mRNA  
 sequence.  
 ACCESSION AV466643 GI:21182599  
 VERSION AV466643.1  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare.  
 ORGANISM Hordeum vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae

REFERENCE 1 (bases 1 to 480)  
 Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.  
 Barley EST's  
 Unpublished (2002)  
 Contact: Schulman AH  
 Institute of Biotechnology  
 University of Helsinki  
 P.O.Box 56 (Vikinkari 6A), University of Helsinki FIN-00014,  
 Finland.  
 Location/Qualifiers  
 1..480  
 /organism="Hordeum vulgare"  
 /db\_xref="taxon:4513"



/clone="S0000800211A09F1"  
/clone\_lib="S00008"  
/tissue\_type="Callus"  
/note="Callus K19"

BASE COUNT 85 a 145 c 145 g 105 t

Query Match 3.7%; Score 23; DB 9; Length 480;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37

Db 175 GCGCCCCCAAGTTCATCCGCAAG 197

RESULT 8  
LOCUS B1777193 505 bp mRNA linear EST 23-JUL-2002

DEFINITION EBr003\_S0002\_F16\_R root, 3 week, waterlogged, cv Optic, EBr003  
Hordeum vulgare cDNA clone EBr003\_S0002\_F16 5', mRNA sequence.

ACCESSION B1777193 GI:21948326

KEYWORDS EST.

SOURCE Hordeum vulgare.

ORGANISM Hordeum vulgare.

REFERENCE 1 (bases 1 to 505)

AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,  
Ramsay, L., Machray, G., Marshall, D.F.M. and Maugh, R.

TITLE Development of Barley Transcriptome Resources

JOURNAL Unpublished (2001)

COMMENT On Sep 26, 2001 this sequence version replaced gi:15780085.

CONTACT: Maugh R, Marshall DF

Genome Dynamics/Computational Biology

Scottish Crop Research Institute

Invergowrie, Dundee, DD2 5DA, Scotland, UK

Tel: 00 44 1382 562731

Fax: 00 44 1382 562426

Email: est@scri.sari.ac.uk

All sequence has a Phred quality score of 20 or over

Seq primer: M13 reverse.

location/Qualifiers

1..505

/organism="Hordeum vulgare"

/cultivar="Optic"

/db\_xref="taxon:4513"

/clone="EBr003\_S0002\_F16"

/clone\_lib="root, 3 week, waterlogged, cv Optic, EBr003"

/tissue\_type="root"

/dev\_stage="3 week"

/lab\_host="DH10B"

/note="Vector: pSPORT1, Site 1: Sal I; Site 2: Not I;  
Non-normalised library, directionally cloned into pSPORT1.  
Derived from roots of 3 week old waterlogged barley  
plants. Developed as part of the barley transcriptome  
resources of BBSRC/SEERAD funded cereal IGF (Investigating  
Gene Function) Project."

BASE COUNT 92 a 147 c 157 g 109 t

ORIGIN

Query Match 3.7%; Score 23; DB 13; Length 505;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37

Db 171 GCGCCCCCAAGTTCATCCGCAAG 193

RESULT 9

AV926845 553 bp mRNA linear EST 18-JAN-2002  
LOCUS AV926845 K. Sato unpublished cDNA library, cv. Haruna Nijo second  
DEFINITION leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA  
clone basd23p19 5', mRNA sequence.

ACCESSION AV926845 GI:18222642

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare.

ORGANISM Hordeum vulgare subsp. vulgare.

REFERENCE 1 (bases 1 to 553)

AUTHORS Sato, K., Saito, D. and Takeda, K.

TITLE Barley EST sequencing project in NIG and Okayama Univ

JOURNAL Unpublished (2002)

COMMENT Contact: Tadao Shin-i

Center For Genetic Resource Information

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Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

location/Qualifiers

1..553

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Haruna Nijo"

/db\_xref="taxon:112509"

/clone="basd23p19"

/clone\_lib="K. Sato unpublished cDNA library, cv. Haruna

Nijo second leaf stage seedling leaves"

/tissue\_type="seedling leaves"

/dev\_stage="second leaf stage"

BASE COUNT 102 a 159 c 169 g 123 t

ORIGIN

Query Match 3.7%; Score 23; DB 10; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37

Db 179 GCGCCCCCAAGTTCATCCGCAAG 201

RESULT 10

LOCUS BF277692 559 bp mRNA linear EST 07-MAR-2001

DEFINITION GA\_Eb0031E13f Gossypium arboreum 7-10 dpa fiber library Gossypium

arboreum cDNA clone GA\_Eb0031E13f, mRNA sequence.

ACCESSION BF277692

KEYWORDS EST.

SOURCE Gossypium arboreum.

ORGANISM Gossypium arboreum.

REFERENCE 1 (bases 1 to 559)

AUTHORS Wang, R.A., Fritsch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry

D., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution

of the cotton fiber

Unpublished (2000)

CONTACT: Wang RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rtwing@clemson.edu

Seq primer: TATACGACTCACTATAGG

High quality sequence start: 4  
High quality sequence stop: 557.  
Location/Qualifiers  
1. 559

FEATURES  
source  
/organism="Gossypium arboreum"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Eb0031E13f"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/tissue\_type="Fibers isolated from bolls harvested 7-10 dpa"  
/lab\_host="E. coli"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"  
BASE COUNT  
104 a 166 c 172 g 117 t

Query Match 3.7%; Score 23; DB 12; Length 559;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37  
|||||  
Db 246 GCGCCCCCAAGTTCATCCGCAAG 268

RESULT 11  
BU210608 581 bp mRNA linear EST 04-APR-2002  
LOCUS BU210608 Y. Ogihara unpublished cDNA library, Wb Triticum aestivum  
DEFINITION cDNA clone wh28m18 5', mRNA sequence.  
ACCESSION BU210608  
VERSION BU210608.1 GI:19949310  
KEYWORDS EST.  
SOURCE bread wheat.  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticaceae; Triticum.  
1 (bases 1 to 581)  
Ogihara, Y. and Murai, K.  
Expressed genes in Triticum aestivum  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.  
Location/Qualifiers  
1. 581  
/organism="Triticum aestivum"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="wh28m18"  
/clone\_lib="Y. Ogihara unpublished cDNA library, Wb"  
/tissue\_type="spike at meiosis"  
/dev\_stage="Feekes' scale 9"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
Site 1: EcoRI; Site 2: XhoI; plants were grown under  
hydroponic conditions at UC Davis, salt stressed for 12  
hours, and for 7 days, then dissected and frozen (Akhunov  
in U. Dvorak lab). Total RNA was prepared from sheath  
tissue, equal quantities of RNA were pooled from the two  
samples, polyA was purified from the pooled RNA, a cDNA  
library was made, and the cDNA clones were in vivo  
excised to give plasmid phagemids in the 10 Close lab  
at the University of California, Riverside (Akhunov, Chin  
, Choi, Close, Fenton, Kitanian, Otto, Simons, Zhang).  
Plasmid DNA preparations and DNA sequencing were  
performed in the OD Anderson lab (all other authors)."

BASE COUNT  
114 a 162 c 186 g 119 t

## ORIGIN

Query Match 3.7%; Score 23; DB 13; Length 581;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37  
|||||  
Db 202 GCGCCCCCAAGTTCATCCGCAAG 224

RESULT 12  
AV924875 597 bp mRNA linear EST 18-JAN-2002  
LOCUS AV924875 K. Sato unpublished cDNA library, cv. Haruna Nijo second  
DEFINITION leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA  
clone baad17e17 5', mRNA sequence.  
ACCESSION AV924875  
VERSION AV924875.1 GI:18220654  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare.  
ORGANISM Hordeum vulgare subsp. vulgare.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticaceae; Hordeum.  
1 (bases 1 to 597)  
Sato, K., Saitoh, D. and Takeda, K.  
Barley EST sequencing project in NIG and Okayama Univ  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.  
Location/Qualifiers  
1. 597  
/organism="Hordeum vulgare subsp. vulgare"  
/cultivar="Haruna Nijo"  
/db\_xref="taxon:112509"  
/clone="baad17e17"  
/clone\_lib="K. Sato unpublished cDNA library, cv. Haruna  
Nijo second leaf stage seedling leaves"  
/tissue\_type="seedling leaves"  
/dev\_stage="second leaf stage"

BASE COUNT  
113 a 166 c 186 g 130 t 2 others

Query Match 3.7%; Score 23; DB 10; Length 597;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37  
|||||  
Db 148 GCGCCCCCAAGTTCATCCGCAAG 170

RESULT 13  
AV925509 621 bp mRNA linear EST 18-JAN-2002  
LOCUS AV925509 K. Sato unpublished cDNA library, cv. Haruna Nijo second  
DEFINITION leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA  
clone baad24j08 5', mRNA sequence.  
ACCESSION AV925509  
VERSION AV925509.1 GI:18221288  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare.  
ORGANISM Hordeum vulgare subsp. vulgare.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticaceae; Hordeum.  
1 (bases 1 to 621)

AUTHORS Sato, K., Saitoh, D. and Takeda, K.  
 TITLE Barley EST sequencing project in NIG and Okayama Univ  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp.  
 Location/Qualifiers

FEATURES  
 source  
 1. .621  
 /organism="Hordeum vulgare subsp. vulgare"  
 /cultivar="Haruna NiJo"  
 /db\_xref="taxon:112509"  
 /clone\_1fb="K. Sato unpublished cDNA library, cv. Haruna  
 NiJo second leaf stage seedling leaves"  
 /tissue\_type="seedling leaves"  
 /dev\_stage="second leaf stage"  
 /db\_xref="taxon:112509"  
 /clone\_1fb="K. Sato unpublished cDNA library, cv. Haruna  
 NiJo second leaf stage seedling leaves"  
 /tissue\_type="seedling leaves"  
 /dev\_stage="second leaf stage"

BASE COUNT 112 a 180 c 188 g 141 t  
 ORIGIN

Query Match 3.7%; Score 23; DB 10; Length 621;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37  
 ||||||||||||||||||||||||  
 Db 200 GCGCCCCCAAGTTCATCCGCAAG 222

RESULT 14  
 LOCUS B0739844 655 bp mRNA linear EST 16-JUL-2002  
 DEFINITION B04012 HB Hordeum vulgare cDNA clone HB04D12 similar to 1)  
 Phospholipase D 1 precursor (PLD 1) (Choline phosphatase 1)  
 (Phosphatidylcholine-hydrolyzing phospholipase D 1)  
 g1|7489548|p1|T03402 probable phospholipase D (EC 3.1.4.4), mRNA  
 sequence.  
 B0739844  
 B0739844.1 GI:21684651  
 EST.  
 Hordeum vulgare.  
 SOURCE Hordeum vulgare  
 ORGANISM Hordeum vulgare; Streptophyta; Embryophyta; Tracheophyta;  
 Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 Triticeae; Hordeum.  
 1 (bases 1 to 655)  
 Ozturk, N.Z., Michalowski, C.B., Brazille, S., Borchert, C., Palacio, C.,  
 Normand, C., Murphy, C., Kelley, R., Sant, S.A., McLaughlin, H.,  
 Fredricksen, M.A. and Bohner, H.J.  
 Monitoring large-scale changes in transcript abundance in drought-  
 and salt-stressed barley  
 Unpublished (2002)  
 Contact: Mark Fredricksen  
 Department of Plant Biology  
 University of Illinois  
 1201 W. Gregory Dr., Urbana, IL 61801, USA  
 Tel: 2172655473  
 Email: bohnerlab@life.uiuc.edu.  
 Location/Qualifiers

FEATURES  
 source  
 1. .655  
 /organism="Hordeum vulgare"  
 /strain="cv tokak"  
 /db\_xref="taxon:4513"  
 /clone\_1fb="HB04D12"  
 /clone\_1fb="HB"  
 /tissue\_type="Leaf"  
 /dev\_stage="3 week old"  
 /note="6 and 10 hour drought stress by placing plants on  
 moist paper (75% rel. humidity) in light"  
 BASE COUNT 131 a 177 c 205 g 141 t 1 others

ORIGIN

Query Match 3.7%; Score 23; DB 14; Length 655;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37  
 ||||||||||||||||||||||||  
 Db 162 GCGCCCCCAAGTTCATCCGCAAG 184

RESULT 15  
 LOCUS B1954591 663 bp mRNA linear EST 19-OCT-2001  
 DEFINITION HVSMEM0018U23f Hordeum vulgare green seedling EST library  
 HVCDNA0014 (Blumeria infected) Hordeum vulgare cDNA clone  
 HVSMEM0018U23f, mRNA sequence.  
 B1954591  
 B1954591.1 GI:16300226  
 EST.  
 Hordeum vulgare.  
 SOURCE Hordeum vulgare  
 ORGANISM Hordeum vulgare; Streptophyta; Embryophyta; Tracheophyta;  
 Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 Triticeae; Hordeum.  
 1 (bases 1 to 663)  
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,  
 Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons  
 J., Oates, R. and Main, D.  
 Development of a genetically and physically anchored EST resource  
 for barley genomics: Blumeria infected Morex (compatible) seedling  
 cDNA library  
 Unpublished (2001)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total hg bases = 563  
 Seq primer: AATTACCTCTCACTAAGG  
 High quality sequence stop: 633.  
 Location/Qualifiers

FEATURES  
 source  
 1. .663  
 /organism="Hordeum vulgare"  
 /cultivar="Morex"  
 /db\_xref="taxon:4513"  
 /clone\_1fb="HVSMEM0018U23f"  
 /clone\_1fb="Hordeum vulgare green seedling EST library  
 HVCDNA0014 (Blumeria infected)"  
 /tissue\_type="green seedling leaf"  
 /lab\_host="TUC121"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
 XhoI; Morex (mla) plants were greenhouse grown in the R  
 wise lab at Iowa State University, Ames, IA; 7 day old  
 green seedlings were infected with isolate 5874 of  
 Blumeria graminis f. sp. hordei, and leaves were harvested  
 24, 48 and 72 hr post-inoculation and snap frozen (wise).  
 In the TUC Close lab at the University of California,  
 Riverside, total RNA was prepared from each sample pool,  
 equal quantities of all three RNA pools were combined,  
 poly(A) RNA was purified from the mixture, one primary  
 unamplified cDNA library was made, and 1 million pfu were  
 in vivo excised to give pBluescript SK(-) cDNA phagemids  
 (Chin). Phagemids were plated and picked at the Clemson  
 University Genomics Institute (CUGI) (Begum, Palmer,  
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
 sequencing and sequence analysis were performed at CUGI  
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
 The sequence has been trimmed to remove vector sequence  
 and contains a minimum of 100 bases of phred value 20 or  
 above. For more details on library preparation and

Fri Apr 4 08:49:34 2003

us-09-856-725-2.oligo.rst

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sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
this clone see <http://www.genome.clemson.edu/orders> Also  
see Close TV, Wang R, Kleinholz A, Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30.  
(<http://wheat.pw.usda.gov/gnpages/dgn/31/cover.html>)"

BASE COUNT 139 a 184 c 190 g 150 t

ORIGIN

Query Match 3.7%; Score 23; DB 13; Length 663;  
Best Local Similarity 100.0%; Pred.No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGCCCCCAAGTTCATCCGCAAG 37  
|||  
Db 91 GCGCCCCCAAGTTCATCCGCAAG 113

Search completed: April 3, 2003, 13:27:47  
Job time : 1525 secs